

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: BUKH, J., MILLER, R.H. AND
PURCELL, R.H.
- (ii) TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND
VACCINES
- (iii) NUMBER OF SEQUENCES: 263
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: 26-MAY-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/290,665
(B) FILING DATE: 15-AUG-1994
- (viii) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/086,428
(B) FILING DATE: 29-JUNE-1993
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: RICHARD W. BORK
(B) REGISTRATION NUMBER: 36,459
(C) REFERENCE/DOCKET NUMBER: 2026-4116US2
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(A) TELEPHONE: (212) 758-4800
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(C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAC TCG AGT ATC GTG TAC GAG GCG GCC	78
	GAT GCC ATC CTG CAC ACT CCG GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GTC TCG AGG TGT TGG GTG GCG ATG ACC	156
	CCC ACG GTG GCC ACC AGG GAT GGC AAA CTC CCC ACA GCG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTC GTC GGG AGT GCC	234
	ACC CTC TGT TCG GCC CTC TAG GTG GGG GAC CTG TGC GGG	273
15	TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC	312
	AGG CGC CAC TGG ACG ACG CAA GGC TGC AAT TGT TCT ATC	351
	TAT CCT GGC CAT ATA ACG GGT CAC CGC ATG GCG TGG GAT	390
	ATG ATG ATG AAC TGG TCC CCT ACC ACG GCG TTG GTA GTA	429
	GCT CAG CTG CTC CGG ATC CCG CAA GCC ATC TTG GAC ATG	468
	ATC GCT GGT GCT CAC TGG GGA GTC CTG GCG GGC ATA GCG	507
	TAT TTT TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA	546
20	GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG	576

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30	TAC CAA GTA CGC AAC TCC TCG GGC CTC TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC	78
	GAT GCC ATC CTG CAT TCT CCA GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GCC TCG AAA TGT TGG GTG GCG GTG GCC	156
	CCC ACG GTG GCC ACC AGG GAC GGC AAG CTC CCC GCA ACG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC	234
35	ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC TTG TGC GGG	273

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	TCT	GTC	TTC	CTT	GTC	GGC	CAA	CTG	TTC	ACC	TTC	TCC	CCC	312
	AGA	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAC	TGT	TCT	ATC	351
	TAC	CCC	GGC	CAT	ATT	ACG	GGT	CAT	CGC	ATG	GCG	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	GCA	GCG	CTG	GTA	ATG	429
	GCG	CAG	CTG	CTC	AGG	ATC	CCG	CAG	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
5	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	GTG	GTG	546
	GTA	CTG	TTG	CTG	TTT	ACC	GGC	GTC	GAT	GCG				576

(2) INFORMATION FOR SEQ ID NO:3:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DR1

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20

	CAC	CAA	GTG	CGC	AAC	TCT	ACA	GGG	CTT	TAC	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAT	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	GCG	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GCC	TCG	AGG	TGT	TGG	GTG	GCG	GTG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	195
20	CAG	CTT	CGA	CGT	CAC	ATC	GAC	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAC	GTG	GGG	GAC	CTG	TGC	GGG	273
	TCT	GTC	TTC	CTT	GTC	GGT	CAA	CTG	TTC	ACC	TTT	TCT	CCC	312
	AGG	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAT	CCC	GGC	CAT	ATA	ACG	GGA	CAC	CGT	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACA	GCG	CTG	GTA	ATG	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAC	ATG	468
25	ATC	GCT	GGA	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	GTG	GTA	546
	GTG	CTG	TTG	CTG	TTT	GCC	GGC	GTT	GAT	GCG				576

(2) INFORMATION FOR SEQ ID NO:4:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DR4

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	CAC	CAA	GTG	CGC	AAC	TCT	ACA	GGG	CTT	TAC	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAT	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	ACG	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
5	CGC	GAG	GGT	AAC	ACC	TCG	AGG	TGT	TGG	GTG	GCG	GTG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	195
	CAG	CTC	CGA	CGT	CAC	ATC	GAC	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAC	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTC	CTT	GTC	GGT	CAA	CTG	TTC	ACC	TTC	TCT	CCC	312
	AGG	CAC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAT	TGT	TCC	ATC	351
	TAT	CCC	GGC	CAT	ATA	ACG	GGC	CAC	CGC	ATG	GCG	TGG	GAT	390
10	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACA	GCG	CTG	GTA	GTA	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	GTA	546
	GTG	CTG	TTG	CTG	TTT	GCC	GGC	GTT	GAT	GCG				576

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	TAC	CAA	GTG	CGC	AAC	TCC	ACG	GGG	CTT	TAC	CAT	GTT	ACC	39
	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATT	GTG	TAC	GAG	ACA	GCT	78
	GAT	GCT	ATC	CTA	CAC	GCT	CCG	GGA	TGT	GTC	CCT	TGC	GTT	117
25	CGT	GAG	GGT	AAC	ACC	TCG	AGG	TGT	TGG	GTG	GCG	ATG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	GCA	ACG	195
	CAG	CTT	CGA	CGT	TAC	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGT	TCG	GCC	CTC	TAC	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTT	CTT	GTC	GGT	CAG	CTG	TTT	ACC	TTC	TCT	CCC	312
	AGG	CGC	CTC	TGG	ACG	ACG	CAA	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAT	CCC	GGC	CAT	ATA	ACG	GGT	CAT	CGC	ATG	GCA	TGG	GAT	390
30	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACG	GCA	CTG	GTA	GTA	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAT	ATG	468
	ATC	GCT	GGT	GCT	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGA	AAC	TGG	GCG	AAG	GTC	CTA	GTG	546
	GTG	CTG	CTG	CTA	TTC	GCC	GGC	GTT	GAC	GCG				576

(2) INFORMATION FOR SEQ ID NO:6:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10	TAC CAA GTA CGC AAC TCC ACG GGC CTT TAC CAT GTC ACC	39
	AAT GAC TGC CCT AAC TCG AGC ATT GTG TAC GAG ACG GCC	78
	GAT ACC ATC CTA CAC TCT CCG GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GCC TCG AGA TGT TGG GTG CCG GTG GCC	156
	CCC ACA GTT GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTT GGG AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC CTG TGC GGG	273
	TCT GTC TTT CTT GTC AGC CAG CTG TTC ACT ATC TCC CCC	312
15	AGG CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC	351
	TAC CCC GGC CAT ATA ACG GGT CAC CGT ATG GCA TGG GAT	390
	ATG ATG ATG AAC TGG TCC CCT ACA ACG GCG TTG GTA ATA	429
	GCT CAG CTG CTC AGG GTC CCG CAA GCC GTC TTG GAC ATG	468
	ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG	507
	TAT TTC TCC ATG GCG GGG AAC TGG GCG AAG GTC CTG CTA	546
	GTG CTG TTG CTG TTT GCC GGC GTC GAT GCG	576

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30	TAC CAA GTA CGC AAC TCC TCG GGC CTT TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACG GCC	78
	GAT GCC ATT CTA CAC TCT CCA GGG TGT GTC CCT TGC GTT	117
	CGC GAG GAT GGC GCC CCG AAG TGT TGG GTG GCG GTG GCC	156
	CCC ACA GTC GCC ACT AGG GAC GGC AAA CTC CCT GCA ACG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGA AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG	273
35	TCT GTC TTT CTC GTC AGT CAA CTG TTC ACG TTC TCC CCC	312

AGG CGC CAC TGG ACA ACG CAA GAC TGT AAC TGT TCT ATC 351
 TAT CCC GGC CAC ATA ACG GGT CAC CGC ATG GCA TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCC ACA ACA GCG CTG GTA GTA 429
 GCT CAG CTG CTC AGG ATC CCG CAA GCC GTC TTG GAC ATG 468
 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG ATA 546
 5 GTG CTG TTG CTG TTT TCC GGC GTC GAT GCG 576

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US11

 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAC CAA GTA CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC 39
 AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC 78
 GAT GCC ATC CTG CAC ACT CCG GGG TGT GTT CCT TGC GTT 117
 CGC GAG GGT AAC GCT TCG AGG TGT TGG GTG GCG ATG ACC 156
 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG 195
 CAA CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC 234
 20 ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG 273
 TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC 312
 AGA CGC CAC TGG ACG ACG CAG GGC TGC AAT TGT TCT ATC 351
 TAT CCC GGC CAT ATA ACG GGT CAC CGC ATG GCA TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCT ACG GCG GCG TTG GTG GTA 429
 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468
 ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 25 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546
 GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D1

 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGT	TCC	AAC	TCG	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GAC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	GGC	AAC	GTC	CCC	ACT	ACG	195
5	GCG	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	CTC	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACG	GTA	CAG	GAG	TGT	AAT	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTG	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	TTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGG	GTC	CTG	GCG	GGC	CTC	GCC	507
10	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCT	GGC	GTT	GAC	GGC				576

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAA	GTC	ACC	39
	AAT	GAC	TGT	TCC	AAC	TCG	AGC	ATC	GTG	TAT	GAG	ACA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GAC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	AGC	AGC	GTC	CCC	ACT	ACG	195
25	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGG	GAT	CTT	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAA	TGT	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTG	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
30	GTG	GCG	GGG	GCC	CAC	TGG	GGG	GTC	CTG	GCG	GGC	CTC	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCT	GGC	GTC	GAC	GGC				576

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAC	GTC	ACA	39
AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAG	GCA	GTG	78
GAC	GTG	ATC	ATG	CAT	ACC	CCA	GGG	TGC	GTG	CCC	TGC	GTT	117
CGG	GAG	AAC	AAC	CAC	TCC	CGT	TGC	TGG	GTA	GCG	CTC	ACC	156
CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACG	195
ACA	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	273
TCC	GTT	TTC	CTC	GTC	TCT	CAG	CTG	TTC	ACC	TTT	TCA	CCT	312
CGC	CGG	CAT	GAG	ACA	GCA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
TAT	CCC	GGC	CAC	GTT	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	CTA	GTG	CTA	429
TCG	CAG	TTA	CTC	CGA	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507
TAC	TAC	TCC	ATG	GCG	GGG	AAC	TGG	GCC	AAG	GTT	TTA	ATT	546
GTG	TTG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGC	GTC	GTG	TAT	GAG	ACA	GCA	78
GAC	ATG	ATC	ATG	CAT	ACC	CCT	GGA	TGC	GTG	CCC	TGC	GTA	117
CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGT	TGG	GTA	GCG	CTC	ACT	156
CCC	ACG	CTC	GCG	GCC	AGG	AAC	GTC	AGC	GTC	CCC	ACC	ACG	195
ACA	ATA	CGA	CGT	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
GCC	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTT	TCG	CCT	312
CGC	CGA	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	CTC	351
TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390

ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	GCA	GCC	CTA	GTG	GTG	429
TCG	CAA	TTA	CTC	CGG	ATC	CCG	CAA	GCT	GTC	GTG	GAC	ATG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
TAC	TAT	TCC	ATG	GTG	GGA	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
GTG	ATG	CTA	CTT	TTT	GCC	GGC	GTT	GAT	GGG				576

5 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAT	GAA	GTG	CAC	AAC	GTA	TCC	GGG	ATC	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
GAC	ATG	ATC	ATG	CAT	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTC	117
CGG	GAG	AAC	AAC	TCC	TCC	CGT	TGC	TGG	GTA	GCG	CTC	ACT	156
CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACG	195
ACA	ATA	CGA	CGC	CAT	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGA	GAT	CTC	TGC	GGA	273
TCT	GTC	TTC	CTC	GTC	TCC	CAG	TTG	TTC	ACC	TTC	TCG	CCT	312
CGC	CGG	CAT	GAG	ACG	GTA	CAG	GAC	TGC	AAT	TGC	TCA	ATC	351
TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
TCG	CAG	TTA	CTC	CGA	CTC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
GTG	GCG	GGA	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCT	507
TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCC	AAG	GTT	TTG	ATT	546
GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

25 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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0	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTA	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TTA	AGC	ATC	GTG	TAC	GAG	ACA	ACG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCT	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAA	AAC	AAC	TCC	TCC	CGT	TGT	TGG	GTA	GCG	CTC	GCC	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	195
	GCA	ATA	CGA	CGC	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
5	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTT	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGC	CGA	CAC	GAG	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTA	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCG	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTA	GCG	GGG	GCC	CAC	TGG	GGG	GTC	CTG	GCG	GGC	CTT	GCC	507
10	TAC	TAT	TCC	ATG	GTG	GGA	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTT	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAA	ACA	GCG	78
	GAC	ATG	ATT	ATG	CAT	ACC	CCT	GGA	TGC	ATG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	GTC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
25	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTT	TCG	CCT	312
	CGC	CGA	CAC	GAG	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	ACA	GCC	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCG	CAA	GCT	ATC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
30	TAC	TAT	TCC	ATG	GTG	GGC	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTG	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACT	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GGC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
10	CCC	ACT	CTC	GCG	GCC	AGG	AAC	GCC	AGC	GTC	TCC	ACC	ACG	195
	ACA	ATA	CGA	CAC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTA	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCG	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCC	ATC	351
	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCC	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
15	TCG	CAG	TTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAT	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	ATC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTA	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

	TAT	GAG	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GGC	AAC	TTC	TCT	AGT	TGC	TGG	GTA	GCG	CTC	ACT	156
30	CCC	ACT	CTC	GCG	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCG	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCC	ATC	351
	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
35	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCG	GCC	CTA	GTG	GTA	429

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(i)

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

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(i)

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S9

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	AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAC	GAG	GCA	GCG	78
	GAC	GTG	ATC	ATG	CAT	ACC	CCC	GGG	TGT	GTA	CCC	TGC	GTT	117
	CAG	GAG	GGT	AAC	TCC	TCC	CAA	TGC	TGG	GTG	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCT	ACC	GTC	CCC	ACC	ACG	195
	ACA	ATA	CGA	CGT	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GTT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTG	TGC	GGA	273
5	TCT	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCC	312
	CGT	CGG	CAT	GAG	ACA	GTA	CAG	AAC	TGC	AAT	TGC	TCA	ATC	351
	TAT	CCC	GGA	CAC	GTG	ACA	GGT	CAT	CGC	ATG	GCC	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACA	GCC	CTA	GTG	GTA	429
	TCG	CAG	CTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAT	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
10	GTG	ATG	CTA	CTT	TTT	GCT	GGT	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

20	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GCG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GTG	78
	GAC	GTG	ATC	CTG	CAC	ACC	CCT	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	TCC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGT	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
25	TCT	GTT	TTC	CTT	GTT	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGT	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGT	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTA	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	GCA	GCC	TTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	CTG	ATT	546
30	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA10

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	TCC	AGC	GTC	CCC	ACT	ACG	195
10	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGC	CGG	TAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCA	ATC	351
	TAT	CCC	GGC	CGC	GTA	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCT	CTA	GTA	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	ATC	GTG	GAC	ATG	468
15	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTT	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:22:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW2

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAT	CAT	GTC	ACG	39
	AAC	GAC	TGT	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
	GAC	ATG	ATC	ATG	CAT	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GCC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
30	CCC	ACG	CTA	GCA	GCC	AGG	AAC	ACC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GTT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACT	TTT	TCA	CCT	312
	CGC	CGG	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGT	TCC	ATC	351
	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTG	GTG	GTA	429
35	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468

GTA GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCA 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTC TTT GCT GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:23:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAC GAA GTG CGC AAC GTG TCC GGG GTG TAC TAT GTC ACG 39
AAC GAC TGT TCC AAC TCA AGC ATT GTG TAT GAG ACA GCG 78
GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT 117
15 CGG GAG AGC AAT TCC TCC CGC TGC TGG GTA GCG CTT ACT 156
CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACT AAG 195
ACA ATA CGA CGT CAC GTC GAC TTG CTC GTT GGG GCG GCT 234
GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACT TTC TCG CCT 312
CGC CGG CAT GAG ACA GTA CAG GAC TGC AAC TGC TCA ATC 351
TAT CCC GGC CAC GTA ACA GGT CAC CGT ATG GCT TGG GAT 390
20 ATG ATG ATG AAC TGG TCG CCC ACA ACG GCA CTA GTG GTG 429
TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG CTG CTA CTC TTT GCC GGC GTT GAT GGG 576

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGC ATT GTG TTT GAG GCA GCG 78

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	GAC	TTG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GGC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	ACC	AGC	GTC	CCC	ACT	ACG	195
	ACG	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAT	GTG	GGA	GAC	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCT	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
5	CGC	CGG	CAT	GAG	ACT	TTG	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAT	CTG	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACA	GCT	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
	GTG	ACA	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GCG	GGG	AAC	TGG	GCT	AAG	GTT	TTA	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

20	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACT	CCC	GGG	TGC	GTG	CCC	TGT	GTT	117
	CGG	GAG	AAC	AAT	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCT	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	ACT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGG	273
	TCC	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
25	CGT	CAG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGT	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	CTG	ATT	546
	GTG	TTG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5	GCC	CAA	GTG	AGG	AAC	ACC	AGC	CGC	GGT	TAC	ATG	GTG	ACT	39
	AAC	GAC	TGT	TCC	AAT	GAG	AGC	ATC	ACC	TGG	CAG	CTC	CAA	78
	GCC	GCG	GTT	CTC	CAC	GTC	CCC	GGG	TGT	ATC	CCG	TGT	GAG	117
	AGG	CTG	GGA	AAT	ACA	TCC	CGA	TGC	TGG	ATA	CCG	GTC	ACA	156
	CCA	AAC	GTG	GCC	GTG	CGG	CAG	CCC	GGC	GCT	CTT	ACG	CAG	195
	GGC	TTG	CGG	ACG	CAC	ATC	GAC	ATG	GTT	GTG	ATG	TCC	GCC	234
10	ACG	CTC	TGC	TCT	GCC	CTC	TAC	GTG	GGG	GAC	CTC	TGC	GGC	273
	GGG	GTG	ATG	CTC	GCA	GCC	CAG	ATG	TTC	ATT	GTC	TCG	CCG	312
	CGA	CGC	CAC	TGG	TTT	GTG	CAA	GAA	TGC	AAT	TGC	TCC	ATC	351
	TAC	CCC	GGT	ACC	ATC	ACT	GGA	CAC	CGT	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	GCC	ACC	ATG	ATC	CTG	429
	GCG	TAC	GCG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	ATA	GAC	ATC	468
	ATC	GGC	GGG	GCT	CAC	TGG	GGC	GTC	ATG	TTT	GGC	TTG	GCC	507
15	TAC	TTC	TCT	ATG	CAG	GGA	GCG	TGG	GCG	AAG	GTC	ATT	GTC	546
	ATC	CTC	TTG	CTG	GCT	GCT	GGG	GTG	GAC	GCG				576

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

25	GCA	CAA	GTG	AAG	AAC	ACC	ACT	AAC	AGC	TAC	ATG	GTG	ACC	39
	AAC	GAC	TGT	TCT	AAT	GAC	AGC	ATC	ACT	TGG	CAG	CTC	CAG	78
	GCC	GCG	GTC	CTC	CAC	GTC	CCC	GGG	TGT	GTC	CCG	TGC	GAG	117
	AAA	ACG	GGA	AAT	ACA	TCT	CGG	TGC	TGG	ATA	CCG	GTT	TCA	156
	CCA	AAC	GTG	GCC	GTG	CGG	CAG	CCC	GGC	GCC	CTC	ACG	CAG	195
30	GGC	TTG	CGG	ACG	CAC	ATT	GAC	ATG	GTT	GTG	ATG	TCC	GCC	234
	ACG	CTC	TGC	TCT	GCT	CTT	TAC	GTG	GGG	GAC	CTC	TGC	GGC	273
	GGG	GTG	ATG	CTC	GCA	GCC	CAG	ATG	TTC	ATC	GTC	TCG	CCG	312
	CAA	CAT	CAC	TGG	TTT	GTG	CAA	GAC	TGC	AAT	TGC	TCT	ATC	351
	TAC	CCT	GGC	ACC	ATC	ACT	GGA	CAC	CGT	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACG	GCC	ACC	ATG	ATC	CTG	429
	GCG	TAC	GCG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	TTA	GAC	ATC	468
35	GTT	AGC	GGG	GCA	CAC	TGG	GGC	GTC	ATG	TTC	GGC	TTG	GCC	507

TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC 546
ATC CTT CTG CTG GCC GCT GGG GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:28:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
10 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCC GAA GTG AAG AAC ACC AGT AGC AGC TAC ATG GTG ACA 39
AAT GAC TGT TCC AAC GAC AGC ATC ACC TGG CAA CTC CAG 78
GCC GCG GTC CTC CAC GTC CCC GGG TGC GTC CCG TGC GAG 117
AGA GTT GGA AAC GCG TCG CGG TGC TGG ATA CCG GTC TCG 156
15 CCA AAC GTA GCT GTG CAG CGG CCT GGC GCC CTC ACG CAG 195
GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC 234
ACG CTC TGC TCC GCT CTC TAC GTG GGG GAT CTC TGC GGC 273
GGG GTA ATG CTC GCC GCT CAG ATG TTC ATT ATC TCG CCG 312
CAG CAC CAC TGG TTT GTG CAG GAA TGC AAC TGC TCC ATT 351
TAC CCT GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390
ATG ATG ATG AAC TGG TCG CCC ACA ACC ACC ATG ATC TTG 429
20 GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468
ATC AGC GGA GCT CAC TGG GGC GTC ATG TTC GGC CTA GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC GTT GTC 546
ATC CTG TTG CTC ACC GCT GGC GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:29:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
30 (C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTC CAA GTG AAA AAC ACC AGT ACC AGC TAT ATG GTG ACC 39
AAT GAC TGC TCC AAC GAC AGC ATC ACT TGG CAA CTT GAG 78
35 GCT GCG GTC CTC CAC GTT CCC GGG TGT GTC CCG TGC GAG 117

AAA	GTG	GGA	AAT	ACA	TCT	CGG	TGC	TGG	ATA	CCG	GTC	TCA	156
CCA	AAT	GTG	GCC	GTG	CAG	CGG	CCT	GGC	GCC	CTC	ACG	CAG	195
GGC	TTG	CGG	ACT	CAC	ATC	GAC	ATG	GTC	GTG	ATG	TCC	GCC	234
ACG	CTC	TGC	TCC	GCT	CTT	TAC	GTG	GGG	GAC	TTC	TGC	GGT	273
GGG	ATG	ATG	CTC	GCA	GCC	CAA	ATG	TTC	ATT	GTC	TCG	CCG	312
CGC	CAC	CAC	TCG	TTT	GTG	CAG	GAA	TGC	AAC	TGC	TCC	ATC	351
TAC	CCC	GGT	ACC	ATC	ACC	GGG	CAC	CGT	ATG	GCA	TGG	GAC	390
ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACG	GCC	ACT	TTG	ATC	CTG	429
GCG	TAC	GTG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	ATA	GAC	ATC	468
ATT	AGC	GGG	GCG	CAT	TGG	GGC	GTC	TTG	TTC	GGC	TTA	GCC	507
TAC	TTC	TCT	ATG	CAG	GGA	GCG	TGG	GCG	AAA	GTC	GTT	GTC	546
ATC	CTT	CTG	CTA	GCC	GCT	GGG	GTG	GAC	GCG				576

10 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCC	AGC	TAC	TAC	GCC	ACC	39
AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
GAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
AAT	GAC	AAT	GGC	ACC	CTG	CGC	TGC	TGG	ATA	CAA	GTG	ACA	156
CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTT	ACT	CAT	195
AAC	CTG	CGA	ACA	CAC	GTC	GAC	GTG	ATC	GTA	ATG	GCA	GCT	234
ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTA	TGC	GGG	273
GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	CTC	ATA	ATA	TCG	CCT	312
GAA	CGC	CAC	AAC	TTT	ACC	CAG	GAG	TGC	AAC	TGT	TCC	ATC	351
TAC	CAA	GGT	CAT	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTC	429
GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GCC	CTC	CAG	GTT	468
GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
TAT	TTC	TCC	ATG	CAG	GGA	GCG	TGG	GCC	AAA	GTC	ATT	GCC	546
ATC	CTC	CTT	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

30 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

5	GTG	GAA	GTC	AGG	AAC	ACC	AGT	TCT	AGT	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
	AAT	GAC	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAT	ATA	GAT	ATG	ATT	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	GTA	TCG	CCA	312
10	GAA	CAC	CAC	CAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CAC	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
	ATG	ATG	CTT	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
	GCC	TAT	GCC	GCC	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTC	468
	GTC	TTC	GGT	GGT	CAT	TGG	GGT	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAG	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
	ATC	CTC	CTT	CTT	GTA	GCA	GGA	GTG	GAT	GCA				576

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

25	GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCT	AGC	TAC	TAT	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AGC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTC	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCG	TGT	GAG	117
	AAT	GAT	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCG	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAC	GTC	GAT	ATG	ATC	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	ATG	TGC	GGG	273
30	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
	GAA	CGC	CAC	AAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CGT	ATC	ACC	GGC	CAC	CGC	ATG	GCG	TGG	GAC	390
	ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTT	429
	GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTT	468
	GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
35	ATC	CTC	CTG	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

	GTG	GAA	GTT	AGA	AAC	ACC	AGT	TTT	AGC	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCG	AAC	AAC	AGC	ATC	ACC	TGG	CAG	CTC	ACC	78
	AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
	AAT	GAC	AAT	GGC	ACC	TTG	CGC	TGC	TGG	ATA	CAA	GTA	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGT	GGC	GCA	CTC	ACT	CAC	195
	AAC	CTG	CGA	ACG	CAT	GTC	GAC	GTG	ATC	GTA	ATG	GCA	GCT	234
15	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGG	GAC	GTG	TGC	GGG	273
	GCC	GTG	ATG	ATA	GCG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
	GAA	CGC	CAC	AAC	TTC	ACC	CAG	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CAT	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
	ATG	ATG	CTG	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
	GCC	TAC	GCT	GCT	CGT	GTG	CCT	GAA	CTA	GTC	CTT	GAA	GTT	468
	GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
20	TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAA	GTC	ATC	GCC	546
	ATC	CTC	CTC	CTT	GTC	GCA	GGA	GTG	GAC	GCA				576

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

	GTG	GAG	GTC	AAG	GAC	ACC	GGC	GAC	TCC	TAC	ATG	CCG	ACC	39
	AAC	GAT	TGC	TCC	AAC	TCT	AGT	ATC	GTT	TGG	CAG	CTT	GAA	78
	GGA	GCA	GTG	CTT	CAT	ACT	CCT	GGA	TGC	GTC	CCT	TGT	GAG	117
	CGT	ACC	GCC	AAC	GTC	TCT	CGA	TGT	TGG	GTG	CCG	GTT	GCC	156
35	CCC	AAT	CTC	GCC	ATA	AGT	CAA	CCT	GGC	GCT	CTC	ACT	AAG	195

GGC CTG CGA GCA CAC ATC GAT ATC ATC GTG ATG TCT GCT 234
 ACG GTC TGT TCT GCC CTT TAT GTG GGG GAC GTG TGT GGC 273
 GCG CTG ATG CTG GCC GCT CAG GTC GTC GTC GTG TCG CCA 312
 CAA CAC CAT ACG TTT GTC CAG GAA TGC AAC TGT TCC ATA 351
 TAC CCG GGC CGC ATT ACG GGA CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCC ACT ACC ACC ATG CTC CTG 429
 5 GCG TAC TTG GTG CGC ATC CCG GAA GTC ATC TTG GAT ATT 468
 GTT ACA GGA GGT CAT TGG GGT GTA ATG TTT GGC CTC GCT 507
 TAC TTC TCC ATG CAG GGA TCG TGG GCG AAG GTC ATC GTT 546
 ATC CTC CTG CTG ACT GCT GGG GTG GAG GCG 576

(2) INFORMATION FOR SEQ ID NO:35:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
 TTA GAG TGG CGG AAT GTG TCC GGC CTC TAC GTC CTT ACC 39
 AAC GAC TGT TCC AAT AGC AGT ATC GTG TAT GAG GCC GAT 78
 GAC GTC ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT 117
 20 CAG GAC GGC AAT ACA TCT ACG TGC TGG ACC TCA GTG ACG 156
 CCT ACA GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT 195
 TCG ATA CGC AGT CAT GTG GAC CTG CTA GTG GGC GCG GCC 234
 ACG ATG TGC TCT GCG CTC TAC GTG GGT GAT GTG TGT GGG 273
 GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT 312
 CGT CGC CAT CAA ACA GTC CAG ACC TGT AAC TGC TCG CTG 351
 TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT 390
 ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTA 429
 25 GCG CAC GTC CTG CGT CTG CCC CAG ACC TTG TTC GAC ATA 468
 ATA GCT GGG GCC CAT TGG GGC ATC ATG GCG GGC CTA GCC 507
 TAT TAC TCC ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
 ATC ATG GTT ATG TTT TCA GGA GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:36:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 35 (A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

	CTA	GAG	TGG	CGG	AAT	GTG	TCT	GGC	CTC	TAT	GTC	CTT	ACC	39
	AAC	GAC	TGT	CCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
5	GAC	GTC	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	TCG	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCC	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTG	TTA	GTG	GGC	GCG	GCC	234
	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGC	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCG	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
10	TAC	CCA	GGC	CAC	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCC	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTC	CTG	CGG	TTG	CCC	CAG	ACC	TTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCA	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAG	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAT	GCC				576

15 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	CTC	ACC	39
	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
25	GAC	GTT	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGT	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAT	GTC	GGA	GCA	ACC	ACC	GCT	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTA	TTG	GTG	GGC	GCG	GCC	234
	ACT	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTT	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
30	TAC	CCA	GGC	CAT	CTT	TCA	GGA	CAT	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCT	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTT	CTG	CGT	TTG	CCC	CAG	ACC	GTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCG	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAA	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAC	GCC				576

35

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

10	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTT ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT	78
	GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGC AAT ACA TCC ATG TGC TGG ACC CCA GTG ACA	156
	CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC	234
	ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	273
	GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT	312
15	CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG	351
	TAC CCA GGC CAT GTT TCA GGA CAT CGA ATG GCT TGG GAT	390
	ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG	429
	GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA	468
	CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC	507
	TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATT	546
	GTC ATG ATT ATG TTT TCA GGG GTC GAT GCC	576

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT ATC CTT ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT	78
	GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA	156
	CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC	234
	ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	273

GCC GTC TTT CTC GTG GGA CAA GGC TTC ACG TTC AGA CCT 312
 CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG 351
 TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT 390
 ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG 429
 GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA 468
 CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC 507
 5 TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
 ATC ATG ATT ATG TTT TCA GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 10 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z4

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC 39
 AAT GAT TGT CCG AAT TCC AGT ATA GTC TAT GAA GCT GAC 78
 CAT CAC ATC CTA CAC TTG CCG GGG TGC GTA CCC TGT GTG 117
 ATG ACT GGG AAC ACA TCG CGT TGC TGG ACG CCG GTG ACG 156
 CCT ACA GTG GCT GTC GCA CAC CCG GGC GCT CCG CTT GAG 195
 20 TCG TTC CGG CGA CAT GTG GAC TTA ATG GTA GGC GCG GCC 234
 ACT TTG TGT TCT GCC CTC TAT GTT GGG GAC CTC TGC GGA 273
 GGT GCC TTC CTG ATG GGG CAG ATG ATC ACT TTT CGG CCG 312
 CGT CGC CAC TGG ACC ACG CAG GAG TGC AAT TGT TCC ATC 351
 TAC ACT GGC CAT ATC ACC GGC CAG AGG ATG GCG TGG GAC 390
 ATG ATG ATG AAC TGG AGC CCT ACC ACC ACT CTG CTC CTC 429
 GCC CAG ATC ATG AGG GTC CCC ACA GCC TTT CTC GAC ATG 468
 GTT GCC GGA GGC CAC TGG GGC GTC CTC GCG GGC TTG GCG 507
 25 TAC TTC AGC ATG CAA GGC AAT TGG GCC AAG GTA GTC CTG 546
 GTC CTT TTC CTC TTT GCT GGG GTA GAC GCC 576

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z1

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

	GTG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	GTC	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAC	ACC	AGC	ATA	GTG	TAC	GAG	ACG	GAG	78
	CAC	CAC	ATC	ATG	CAC	TTG	CCA	GGG	TGT	GTC	CCC	TGT	GTG	117
	CGG	ACG	GAG	AAT	ACT	TCT	CGC	TGC	TGG	GTG	CCC	TTG	ACC	156
5	CCC	ACT	GTG	GCC	GCG	CCC	TAT	CCG	AAC	GCA	CCG	TTA	GAG	195
	TCC	ATG	CGC	AGG	CAT	GTA	GAC	CTG	ATG	GTG	GGT	GCG	GCT	234
	ACT	ATG	TGT	TCC	GCC	TTC	TAC	ATT	GGA	GAT	CTG	TGT	GGA	273
	GGC	GTC	TTC	CTA	GTG	GGC	CAG	CTG	TTC	GAC	TTC	CGA	CCG	312
	CGC	CGG	CAC	TGG	ACC	ACC	CAG	GAT	TGC	AAC	TGC	TCC	ATC	351
	TAT	CCT	GGT	CAC	GTC	TCG	GGC	CAC	AGG	ATG	GCC	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGC	CCT	ACC	AGC	GCG	CTG	ATT	ATG	429
10	GCT	CAG	ATC	TTA	CGG	ATC	CCC	TCT	ATC	CTA	GGT	GAC	TTG	468
	CTC	ACC	GGG	GGT	CAC	TGG	GGA	GTT	CTT	GCT	GGT	CTA	GCT	507
	TTC	TTC	AGC	ATG	CAG	AGT	AAC	TGG	GCG	AAG	GTC	ATC	CTG	546
	GTC	CTA	TTC	CTC	TTT	GCC	GGG	GTC	GAG	GGA				576

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

	GTT	AAC	TAT	CGC	AAT	GCC	TCG	GGC	GTC	TAT	CAC	GTC	ACC	39
	AAC	GAC	TGC	CCG	AAC	TCG	AGC	ATA	GTG	TAT	GAG	GCC	GAA	78
	CAC	CAG	ATC	TTA	CAC	CTC	CCA	GGG	TGC	TTG	CCC	TGT	GTG	117
	AGG	GTT	GGG	AAT	CAG	TCA	CGC	TGC	TGG	GTG	GCC	CTT	ACT	156
25	CCC	ACC	GTG	GCG	GTG	TCT	TAT	ATC	GGT	GCT	CCG	CTT	GAC	195
	TCC	CTC	CGG	AGA	CAT	GTG	GAC	CTG	ATG	GTG	GGC	GCC	GCT	234
	ACT	GTA	TGC	TCT	GCC	CTC	TAC	GTT	GGA	GAT	CTG	TGC	GGT	273
	GGT	GCA	TTC	TTG	GTT	GGC	CAG	ATG	TTC	TCC	TTC	CAG	CCG	312
	CGA	CGC	CAC	TGG	ACT	ACG	CAG	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAC	GCA	GGG	CAT	ATC	ACG	GGC	CAC	AGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGT	CCC	ACA	ACC	ACC	CTG	CTT	CTC	429
30	GCC	CAG	GTC	ATG	AGG	ATC	CCT	AGC	ACT	CTG	GTA	GAT	CTA	468
	CTC	GCT	GGA	GGG	CAC	TGG	GGC	GTC	CTT	GTT	GGG	TTG	GCG	507
	TAC	TTC	AGT	ATG	CAA	GCT	AAT	TGG	GCC	AAA	GTC	ATC	CTG	546
	GTC	CTT	TTC	CTC	TTT	GCT	GGA	GTT	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:43:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	GTC	AAC	TAT	CAC	AAT	GCC	TCG	GGC	GTC	TAT	CAC	ATC	ACC	39
	AAC	GAC	TGC	CCG	AAC	TCG	AGC	ATA	ATG	TAT	GAG	GCC	GAA	78
10	CAC	CAC	ATC	CTA	CAC	CTC	CCA	GGG	TGC	GTA	CCC	TGT	GTG	117
	AGG	GAG	GGG	AAC	CAG	TCA	CGC	TGC	TGG	GTG	GCC	CTT	ACT	156
	CCC	ACC	GTG	GCG	GCG	CCT	TAT	ATC	GGT	GCA	CCG	CTT	GAA	195
	TCC	ATC	CGG	AGA	CAT	GTG	GAC	CTG	ATG	GTA	GGC	GCT	GCT	234
	ACA	GTG	TGC	TCC	GCT	CTC	TAC	ATT	GGG	GAC	CTG	TGC	GGT	273
	GGC	GTA	TTT	TTG	GTT	GGT	CAG	ATG	TTT	TCT	TTC	CAG	CCG	312
	CGA	CGC	CAC	TGG	ACT	ACG	CAG	GAC	TGC	AAT	TGT	TCC	ATC	351
15	TAT	GCG	GGG	CAC	GTT	ACA	GGC	CAC	AGA	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGT	CCC	ACA	ACC	ACC	TTG	GTC	CTC	429
	GCC	CAG	GTT	ATG	AGG	ATC	CCT	AGC	ACT	CTG	GTG	GAC	CTA	468
	CTC	ACT	GGA	GGG	CAC	TGG	GGT	ATC	CTT	ATC	GGG	GTG	GCA	507
	TAC	TTC	TGC	ATG	CAA	GCT	AAT	TGG	GCC	AAG	GTC	ATT	CTG	546
	GTC	CTT	TTC	CTC	TAC	GCT	GGA	GTT	GAT	GCC				576

20 (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

	TAC	AAC	TAT	CGC	AAC	AGC	TCG	GGT	GTC	TAC	CAT	GTC	ACC	39
	AAC	GAT	TGC	CCG	AAC	TCG	AGC	ATA	GTC	TAT	GAA	ACC	GAT	78
30	TAC	CAC	ATC	TTA	CAC	CTC	CCG	GGA	TGC	GTT	CCT	TGC	GTG	117
	AGG	GAA	GGG	AAC	AAG	TCT	ACA	TGC	TGG	GTG	TCT	CTC	ACC	156
	CCC	ACC	GTG	GCT	GCG	CAA	CAT	CTG	AAT	GCT	CCG	CTT	GAG	195
	TCT	TTG	AGA	CGT	CAC	GTG	GAT	CTG	ATG	GTG	GGC	GGC	GCC	234
	ACT	CTC	TGC	TCC	GCC	CTC	TAC	ATC	GGA	GAC	GTG	TGT	GGG	273
	GGT	GTG	TTC	TTG	GTC	GGT	CAA	CTG	TTC	ACC	TTC	CAA	CCT	312
35	CGC	CGC	CAC	TGG	ACC	ACC	CAA	GAC	TGC	AAT	TGT	TCC	ATC	351

TAC	ACA	GGA	CAT	ATC	ACA	GGA	CAC	AGA	ATG	GCT	TGG	GAC	390
ATG	ATG	ATG	AAT	TGG	AGC	CCC	ACT	GCG	ACG	CTG	GTC	CTC	429
GCC	CAA	CTT	ATG	AGG	ATC	CCA	GGC	GCC	ATG	GTC	GAC	CTG	468
CTT	GCA	GGC	GGC	CAC	TGG	GGC	ATT	CTG	GTT	GGC	ATA	GCG	507
TAC	TTC	AGC	ATG	CAA	GCT	AAT	TGG	GCC	AAG	GTT	ATC	CTG	546
GTC	CTG	TTT	CTC	TTT	GCT	GGA	GTC	GAC	GCT				576

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTT	CCC	TAC	CGG	AAT	GCC	TCT	GGG	GTT	TAC	CAT	GTC	ACC	39
AAT	GAC	TGC	CCA	AAC	TCC	TCC	ATA	GTC	TAC	GAG	GCT	GAT	78
AGC	CTG	ATC	TTG	CAC	GCA	CCT	GGC	TGC	GTG	CCC	TGT	GTC	117
AGG	CAA	GAT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAA	ATC	ACC	156
CCC	ACA	CTG	TCA	GCC	CCG	ACC	TTC	GGA	GCG	GTC	ACG	GCT	195
CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	TTA	GCG	GGA	GGA	GCT	234
GCT	CTC	TGC	TCC	GCA	CTA	TAC	GTC	GGC	GAC	GCG	TGC	GGG	273
GCA	GTG	TTT	CTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
CGC	CAG	CAT	ACC	ACA	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
TAC	AGT	GGC	CAT	ATC	ACC	GGC	CAC	CGG	ATG	GCT	TGG	GAC	390
ATG	ATG	ATG	AAT	TGG	TCA	CCT	AGG	ACA	GCC	TTG	CTG	ATG	429
GCC	CAG	ATG	CTA	CGG	ATC	CCC	CAG	GTG	GTC	ATA	GAC	ATC	468
ATA	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTT	GCC	GCC	GCA	507
TAC	TTT	GCG	TCG	GCC	GCC	AAC	TGG	GCT	AAG	GTA	GTG	CTG	546
GTT	CTG	TTC	CTG	TTT	GCG	GGG	GTC	GAT	GGC				576

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

	GTT	CCC	TAC	CGA	AAC	GCC	TCT	GGG	GTT	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTT	TAC	GAG	GCT	GAT	78
	AAC	CTG	ATC	TTG	CAT	GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	117
	AGG	CAA	GAT	AAT	GTC	AGT	AAG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACG	TTG	TCA	GCC	CCG	AAT	CTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	TTA	GCG	GGA	GGG	GCT	234
5	GCC	CTC	TGC	TCC	GCA	CTA	TAC	GTC	GGG	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTT	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAC	ACT	ACG	GTG	CAA	GAC	TGC	AAT	TGC	TCT	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACC	GGC	CAC	CGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACG	GCC	TTG	CTG	ATG	429
	GCC	CAG	TTG	CTA	CGG	ATT	CCC	CAG	GTG	GTC	ATC	GAC	ATC	468
	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTT	GCC	GCC	GCA	507
10	TAT	TTC	GCG	TCA	GCG	GCT	AAC	TGG	GCT	AAG	GTT	ATA	CTG	546
	GTC	TTG	TTT	CTG	TTT	GCG	GGG	GTC	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

20	GTC	CCC	TAC	CGA	AAT	GCC	TCT	GGG	GTT	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAC	GAG	GCT	GAT	78
	AAC	CTG	ATT	CTG	CAC	GCA	CCT	GGT	TGC	GTG	CCC	TGT	GTC	117
	AAG	GAA	GGT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACA	TTG	TCA	GCC	CCG	AAC	CTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GTC	GTT	GAC	TAC	TTA	GCG	GGA	GGG	GCT	234
	GCC	CTC	TGC	TCC	GCA	CTA	TAC	GTC	GGG	GAC	GCG	TGC	GGG	273
25	GCA	GTG	TTT	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAT	ACT	ACG	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
	TAC	AGC	GGC	CAT	ATC	ACC	GGC	CAC	CGA	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAG	GTG	CTA	CGG	ATT	CCC	CAA	GTG	GTC	ATT	GAC	ATC	468
	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GTC	GCA	507
	TAC	TTC	GCG	TCA	GCG	GCT	AAC	TGG	GCT	AAG	GTT	GTG	CTG	546
30	GTC	CTG	TTT	CTG	TTT	GCG	GGG	GTC	GAT	GGC				576

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA6

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

	GTT	CCT	TAC	CGG	AAT	GCC	TCT	GGG	GTG	TAT	CAT	GTT	ACC	39
	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCT	GAT	78
	GAC	CTG	ATC	CTA	CAC	GCA	CCT	GGC	TGC	GTG	CCC	TGT	GTC	117
	CGG	AAG	GAT	AAT	GTC	AGT	AGA	TGC	TGG	GTT	CAT	ATC	ACC	156
	CCC	ACA	CTA	TCA	GCC	CCG	AGC	CTC	GGA	GCG	GTC	ACG	GCT	195
10	CCT	CTT	CGG	AGG	GCC	GTT	GAT	TAC	TTG	GCG	GGA	GGG	GCC	234
	GCC	CTG	TGC	TCC	GCG	TTA	TAC	GTC	GGA	GAC	GTG	TGC	GGG	273
	GCA	TTG	TTT	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAT	GCT	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCC	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACT	GGC	CAC	CGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCC	GCG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAA	ATG	CTA	CGG	ATT	CCC	CAG	GTG	GTC	ATT	GAC	ATC	468
15	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GCT	GCA	507
	TAC	TTC	GCG	TCG	GCG	GCT	AAC	TGG	GCT	AAG	GTT	GTG	CTG	546
	GTC	TTG	TTT	CTG	TTT	GCG	GGG	GTT	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA7

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

	GTC	CCC	TAC	CGA	AAT	GCC	TCC	GGG	GTT	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCG	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCT	GAC	78
	AAC	CTG	ATC	CTG	CAC	GCA	CCT	GGT	TGC	GTG	CCC	TGT	GTC	117
	AGA	CAA	AAT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACA	TTG	TCA	GCC	CCG	AAC	CTC	GGA	GCG	GTC	ACG	GCT	195
30	CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	234
	GCC	CTC	TGC	TCC	GCG	CTA	TAC	GTC	GGG	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTT	TTG	GTA	GGC	CAG	ATG	TTC	AGC	TAT	AGG	CCT	312
	CGC	CAG	CAC	ACT	ACG	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACC	GGC	CAC	CGA	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAG	TTG	CTA	CGG	ATT	CCC	CAG	GTG	GTC	ATC	GAC	ATC	468
35	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GCC	GCA	507

TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG 546
GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTT CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC 39
AAT GAT TGC CCA AAC TCT TCC ATC GTC TAC GAG GCT GAT 78
GAC CTG ATC TTA CAC GCA CCT GGT TGC GTG CCC TGT GTT 117
AGG CAG GGT AAT GTC AGT AGG TGG TGG GTC CAG ATC ACC 156
CCC ACA CTG TCA GCC CCG AGC CTC GGA GCG GTC ACG GCT 195
CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGG GGG GCT 234
GCC CTT TGC TCC GCG TTA TAC GTC GGA GAC GCG TGC GGG 273
GCA GTG TTT TTG GTA GGT CAA ATG TTC ACC TAT AGC CCT 312
CGC CGG CAT AAT GTT GTG CAG GAC TGC AAC TGT TCC ATT 351
TAC AGT GGC CAC ATC ACC GGC CAC CGG ATG GCA TGG GAC 390
ATG ATG ATG AAT TGG TCA CCT ACA ACA GCT TTG GTG ATG 429
GCC CAG TTG TTA CGG ATT CCC CAG GTG GTC ATT GAC ATC 468
ATT GCC GGG GCC CAC TGG GGG GTC TTG TTC GCC GCC GCA 507
TAC TAC GCG TCG GCG GCT AAC TGG GCC AAG GTT GTG CTG 546
GTC CTG TTT CTG TTT GCG GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTT ACC TAC GGC AAC TCC AGT GGG CTA TAC CAT CTC ACA 39
AAT GAT TGC CCC AAC TCC AGC ATC GTG CTG GAG GCG GAT 78
GCT ATG ATC TTG CAT TTG CCT GGA TGC TTG CCT TGT GTG 117
AGG GTC GAT GAT CGG TCC ACC TGT TGG CAT GCT GTG ACC 156

	CCC	ACC	CTG	GCC	ATA	CCA	AAT	GCT	TCC	ACG	CCC	GCA	ACG	195
	GGA	TTC	CGC	AGG	CAT	GTG	GAT	CTT	CTT	GCG	GGC	GCC	GCA	234
	GTG	GTT	TGC	TCA	TCC	CTG	TAC	ATC	GGG	GAC	CTG	TGT	GGC	273
	TCT	CTC	TTT	TTG	GCG	GGA	CAA	CTA	TTT	ACC	TTT	CAG	CCC	312
	CGC	CGT	CAT	TGG	ACT	GTG	CAA	GAC	TGC	AAC	TGC	TCC	ATC	351
	TAT	ACA	GGC	CAC	GTC	ACC	GGC	CAC	AGG	ATG	GCT	TGG	GAC	390
5	ATG	ATG	ATG	AAC	TGG	TCA	CCC	ACA	ACC	ACT	CTG	GTC	CTA	429
	TCT	AGC	ATC	TTG	AGG	GTA	CCT	GAG	ATT	TGT	GCG	AGT	GTG	468
	ATA	TTT	GGT	GGC	CAT	TGG	GGG	ATA	CTA	CTA	GCC	GTT	GCC	507
	TAC	TTT	GGC	ATG	GCT	GGC	AAC	TGG	CTA	AAA	GTT	CTG	GCT	546
	GTT	CTG	TTC	CTA	TTT	GCA	GGG	GTT	GAA	GCA				576

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5				10					15	
20	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu
					20				25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Val	Ser
					35				40					45	
	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50				55					60	
	Lys	Leu	Pro	Thr	Ala	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65				70					75	
25	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80				85					90	
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95				100					105	
	Arg	His	Trp	Thr	Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110				115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125				130					135	
30	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro
					140				145					150	
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155				160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170				175					180	

° Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK9

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

15 Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
20 25 30
His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
35 40 45
Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
20 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
25 Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Val Val Val Leu Leu Leu Phe Thr Gly Val Asp Ala
185 190

30

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DR1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

	His	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
					35					40					45	
10	Arg	Cys	Trp	Val	Ala	Val	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
15	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
20	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Val	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:55:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

	His	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	

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0
5
10
15

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(i)

20

(vi)

25 (xi)

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° Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg Leu Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 5 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

20 Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Thr Ile Leu
 20 25 30
 His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
 35 40 45
 Arg Cys Trp Val Pro Val Ala Pro Thr Val Ala Thr Arg Asp Gly
 50 55 60
 25 Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
 65 70 75
 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Ile Ala Gln Leu Leu Arg Val Pro
 140 145 150
 Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165

35

° Ala Gly Ile Ala Tyr Phe Ser Met Ala Gly Asn Trp Ala Lys Val
170 175 180
Leu Leu Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:58:

5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homomapiens
(C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Ala Ile Leu
20 25 30
His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Asp Gly Ala Pro
35 40 45
Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
20 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
25 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Leu Leu Leu Phe Ser Gly Val Asp Ala
185 190
30

(2) INFORMATION FOR SEQ ID NO:59:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
10	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
15	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Trp	Thr	Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
20	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

25 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

35

0	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Gly
					50					55					60
5	Asn	Val	Pro	Thr	Thr	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Ile	Ser	Gln	Leu	Phe	Thr	Leu	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
10	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
15					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:61:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 25 (C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Gln	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
30	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75

35

° Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
5 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
10 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK1

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Val Asp Val Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn His Ser
35 40 45
25 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
30 Arg His Glu Thr Ala Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Leu Ser Gln Leu Leu Arg Ile Pro
140 145 150

35

° Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160
 Ala Gly Leu Ala Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
 185 190

5 (2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

15 Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Val Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
 50 55 60
 20 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 25 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 30 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

35

09084691 052658

(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homocapiens
(C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

His	Glu	Val	His	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp
				5					10					15
Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
				20					25					30
His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
				35					40					45
Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
				50					55					60
Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
				65					70					75
Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
				80					85					90
Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
				95					100					105
Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
				110					115					120
His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
				125					130					135
Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Leu	Pro
				140					145					150
Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
				155					160					165
Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
				170					175					180
Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
				185					190					

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Leu Ser Ile Val Tyr Glu Thr Thr Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 5 Arg Cys Trp Val Ala Leu Ala Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 10 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 15 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:66:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
 5 10 15
 30 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Met Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 35

Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 5 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 10 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 15
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND5
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
 Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Ser Thr Thr Thr Ile Arg His His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 30 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 35

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu
 155 160
 Ala Gly Leu Ala Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

15 Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Phe Ser
 35 40 45
 Ser Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 20 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 25 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu
 155 160 165
 30 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:69:

00034691 052600

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
10	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60
	Ser	Val	Pro	Thr	Thr	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
15	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Leu	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
20	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Ile	Leu	Asp	Val	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
25	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:70:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Val	Ile	Met
					20					25					30
5	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Glu	Gly	Asn	Ser	Ser
					35					40					45
	Gln	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
	Thr	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Val	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
10	Gly	Ser	Val	Phe	Leu	Ile	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asn	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
15	Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Val	Asp	Val	Ile	Leu
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60

Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 5 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 10 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 20 (C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
 Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 30 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg Tyr Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 Arg Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135

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372577_1

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

10	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Tyr	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Ser	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
15	Ser	Val	Pro	Thr	Lys	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
20	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
25	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:75:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp
					5				10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Phe	Glu	Ala	Ala	Asp	Leu	Ile	Met
					20				25						30
5	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ser	Ser
					35				40						45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Thr
					50				55						60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65				70						75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
10					80				85						90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95				100						105
	Arg	His	Glu	Thr	Leu	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110				115						120
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125				130						135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
15					140				145						150
	Gln	Ala	Val	Met	Asp	Met	Val	Thr	Gly	Ala	His	Trp	Gly	Val	Leu
					155				160						165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Ala	Gly	Asn	Trp	Ala	Lys	Val
					170				175						180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185				190						

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

30	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp
					5				10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20				25						30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35				40						45

00004691 052698

° Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Thr Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 5 Gln His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 10 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:77:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 20 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
 Ala Gln Val Arg Asn Thr Ser Arg Gly Tyr Met Val Thr Asn Asp
 5 10 15
 25 Cys Ser Asn Glu Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
 20 25 30
 His Val Pro Gly Cys Ile Pro Cys Glu Arg Leu Gly Asn Thr Ser
 35 40 45
 Arg Cys Trp Ile Pro Val Thr Pro Asn Val Ala Val Arg Gln Pro
 50 55 60
 Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
 65 70 75
 30 Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg
 95 100 105
 Arg His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 35

Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
 140 145 150
 Glu Val Ile Ile Asp Ile Ile Gly Gly Ala His Trp Gly Val Met
 155 160 165
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 5 Ile Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 10 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T4

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ala Gln Val Lys Asn Thr Thr Asn Ser Tyr Met Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
 20 25 30
 His Val Pro Gly Cys Val Pro Cys Glu Lys Thr Gly Asn Thr Ser
 35 40 45
 Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Arg Gln Pro
 50 55 60
 Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
 65 70 75
 Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 25 Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Gln
 95 100 105
 His His Trp Phe Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
 140 145 150
 30 Glu Val Ile Leu Asp Ile Val Ser Gly Ala His Trp Gly Val Met
 155 160 165
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 Val Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
 185 190

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09034691 052699

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

10	Ala	Glu	Val	Lys	Asn	Thr	Ser	Thr	Ser	Tyr	Met	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Gln	Ala	Ala	Val	Leu
					20					25					30
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Arg	Val	Gly	Asn	Ala	Ser
					35					40					45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Gln	Arg	Pro
					50					55					60
15	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Gly	Val	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Ile	Ser	Pro	Gln
					95					100					105
	His	His	Trp	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
20	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro
					140					145					150
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Ser	Gly	Ala	His	Trp	Gly	Val	Met
					155					160					165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
					170					175					180
25	Val	Val	Ile	Leu	Leu	Leu	Thr	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

	Val	Gln	Val	Lys	Asn	Thr	Ser	Thr	Ser	Tyr	Met	Val	Thr	Asn	Asp
					5					10					15
5	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Glu	Ala	Ala	Val	Leu
					20					25					30
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Val	Gly	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Gln	Arg	Pro
					50					55					60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
10	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Phe	Cys
					80					85					90
	Gly	Gly	Met	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Arg
					95					100					105
	His	His	Ser	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
15	Ser	Pro	Thr	Ala	Thr	Leu	Ile	Leu	Ala	Tyr	Val	Met	Arg	Val	Pro
					140					145					150
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Ser	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
					170					175					180
20	Val	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH:	192 amino acids
	(B)	TYPE:	amino acid
25	(C)	STRANDEDNESS:	unknown
	(D)	TOPOLOGY:	unknown

(vi) ORIGINAL SOURCE:

(A)	ORGANISM:	homosapiens
(C)	INDIVIDUAL ISOLATE:	DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

	Val	Glu	Val	Arg	Asn	Ile	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asp	Ala	Val	Leu
					20					25					30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu
					35					40					45

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Arg Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
50 55 60
Gly Ala Leu Thr His Asn Leu Arg Thr His Val Asp Val Ile Val
65 70 75
Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
80 85 90
5 Gly Ala Val Met Ile Val Ser Gln Ala Leu Ile Ile Ser Pro Glu
95 100 105
Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
125 130 135
Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
140 145 150
10 Glu Leu Ala Leu Gln Val Val Phe Gly Gly His Trp Gly Val Val
155 160 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
170 175 180
Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
185 190

15 (2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

25 Val Glu Val Arg Asn Thr Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
5 10 15
Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
20 25 30
His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
35 40 45
His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
50 55 60
30 Gly Ala Leu Thr His Asn Leu Arg Ala His Ile Asp Met Ile Val
65 70 75
Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
80 85 90
Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Val Ser Pro Glu
95 100 105
His His His Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
110 115 120

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His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
 125 130 135
 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
 140 145 150
 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
 155 160 165
 5 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:83:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Val Glu Val Arg Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
 20 20 25 30
 His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
 35 40 45
 His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
 50 55 60
 Gly Ala Leu Thr His Asn Leu Arg Ala His Val Asp Met Ile Val
 65 70 75
 25 Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
 80 85 90
 Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Ile Ser Pro Glu
 95 100 105
 Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
 110 115 120
 Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
 125 130 135
 30 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
 140 145 150
 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
 155 160 165
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val	Glu	Val	Arg	Asn	Thr	Ser	Phe	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	5	10	15
Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu	20	25	30
His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	35	40	45
Arg	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	50	55	60
Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Thr	His	Val	Asp	Val	Ile	Val	65	70	75
Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	80	85	90
Gly	Ala	Val	Met	Ile	Ala	Ser	Gln	Ala	Phe	Ile	Ile	Ser	Pro	Glu	95	100	105
Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	110	115	120
His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	125	130	135
Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	140	145	150
Glu	Leu	Val	Leu	Glu	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	155	160	165
Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	170	175	180
Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				185	190	

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

5	Val	Glu	Val	Lys	Asp	Thr	Gly	Asp	Ser	Tyr	Met	Pro	Thr	Asn	Asp	5	10	15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Trp	Gln	Leu	Glu	Gly	Ala	Val	Leu	20	25	30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Glu	Arg	Thr	Ala	Asn	Val	Ser	35	40	45
	Arg	Cys	Trp	Val	Pro	Val	Ala	Pro	Asn	Leu	Ala	Ile	Ser	Gln	Pro	50	55	60
10	Gly	Ala	Leu	Thr	Lys	Gly	Leu	Arg	Ala	His	Ile	Asp	Ile	Ile	Val	65	70	75
	Met	Ser	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	80	85	90
	Gly	Ala	Leu	Met	Leu	Ala	Ala	Gln	Val	Val	Val	Val	Ser	Pro	Gln	95	100	105
	His	His	Thr	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	110	115	120
15	Arg	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	125	130	135
	Ser	Pro	Thr	Thr	Thr	Met	Leu	Leu	Ala	Tyr	Leu	Val	Arg	Ile	Pro	140	145	150
	Glu	Val	Ile	Leu	Asp	Ile	Val	Thr	Gly	Gly	His	Trp	Gly	Val	Met	155	160	165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ser	Trp	Ala	Lys	Val	170	175	180
20	Ile	Val	Ile	Leu	Leu	Leu	Thr	Ala	Gly	Val	Glu	Ala				185	190	

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

35	Leu	Glu	Trp	Arg	Asn	Val	Ser	Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	5	10	15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	20	25	30

His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
 35 40 45
 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val
 50 55 60
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 65 70 75
 5 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
 95 100 105
 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 10 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
 140 145 150
 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Met
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
 170 175 180
 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
 185 190
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(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
 35 40 45
 30 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val
 50 55 60
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
 95 100 105
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° Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	
					20					25					30	
15	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser	
					35					40					45	
	Met	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val	
					50					55					60	
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ala	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	
					80					85					90	
20	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	
					95					100					105	
	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly	
					110					115					120	
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Ile	Leu	Arg	Leu	Pro	
					140					145					150	
25	Gln	Thr	Leu	Phe	Asp	Ile	Leu	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu	
					155					160					165	
	Ala	Gly	Leu	Ala	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val		
					170					175					180	
	Ala	Ile	Val	Met	Ile	Met	Phe	Ser	Gly	Val	Asp	Ala				
					185					190						

30 (2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

5	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Ile	Leu	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser
					35					40					45
	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val
10					50					55					60
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys
					80					85					90
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg
					95					100					105
	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly
15					110					115					120
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Ile	Leu	Arg	Leu	Pro
					140					145					150
	Gln	Thr	Leu	Phe	Asp	Ile	Leu	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
					155					160					165
20	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Ala	Ile	Ile	Met	Ile	Met	Phe	Ser	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:91:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

35	Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp
					5					10					15

° Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu
 20 25 30
 His Leu Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Thr Ser
 35 40 45
 Arg Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro
 50 55 60
 Gly Ala Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val
 65 70 75
 5 Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Gly Ala Phe Leu Met Gly Gln Met Ile Thr Phe Arg Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Glu Cys Asn Cys Ser Ile Tyr Thr Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 10 Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro
 140 145 150
 Thr Ala Phe Leu Asp Met Val Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Phe Ser Met Gln Gly Asn Trp Ala Lys Val
 170 175 180
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190
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(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z1

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Val His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Thr Ser Ile Val Tyr Glu Thr Glu His His Ile Met
 20 25 30
 His Leu Pro Gly Cys Val Pro Cys Val Arg Thr Glu Asn Thr Ser
 35 40 45
 30 Arg Cys Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Pro
 50 55 60
 Asn Ala Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val
 65 70 75
 Gly Ala Ala Thr Met Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys
 80 85 90
 35

° Val Gly Leu Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
 170 175 180
 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:94:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Asn Tyr His Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Met Tyr Glu Ala Glu His His Ile Leu
 20 25 30
 15 His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile
 50 55 60
 Gly Ala Pro Leu Glu Ser Ile Arg Arg His Val Asp Leu Met Val
 65 70 75
 Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys
 80 85 90
 20 Gly Gly Val Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Thr Leu Val Leu Ala Gln Val Met Arg Ile Pro
 140 145 150
 25 Ser Thr Leu Val Asp Leu Leu Thr Gly Gly His Trp Gly Ile Leu
 155 160 165
 Ile Gly Val Ala Tyr Phe Cys Met Gln Ala Asn Trp Ala Lys Val
 170 175 180
 Ile Leu Val Leu Phe Leu Tyr Ala Gly Val Asp Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 35 (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

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Tyr	Asn	Tyr	Arg	Asn	Ser	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
				5					10					15
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Asp	Tyr	His	Ile	Leu
				20					25					30
His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Lys	Ser
				35					40					45
Thr	Cys	Trp	Val	Ser	Leu	Thr	Pro	Thr	Val	Ala	Ala	Gln	His	Leu
				50					55					60
Asn	Ala	Pro	Leu	Glu	Ser	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val
				65					70					75
Gly	Gly	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Val	Cys
				80					85					90
Gly	Gly	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Gln	Pro	Arg
				95					100					105
Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly
				110					115					120
His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
				125					130					135
Ser	Pro	Thr	Ala	Thr	Leu	Val	Leu	Ala	Gln	Leu	Met	Arg	Ile	Pro
				140					145					150
Gly	Ala	Met	Val	Asp	Leu	Leu	Ala	Gly	Gly	His	Trp	Gly	Ile	Leu
				155					160					165
Val	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Gln	Ala	Asn	Trp	Ala	Lys	Val
				170					175					180
Ile	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala			
				185					190					

(2) INFORMATION FOR SEQ ID NO:96:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

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Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
				5					10					15

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° Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Ser Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser
35 40 45
Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Thr Phe
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
5 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
95 100 105
Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
10 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Met Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
15 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA4

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser
35 40 45
30 Lys Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90

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° Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
 95 100 105
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 5 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

20 Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
 20 25 30
 His Ala Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn Val Ser
 35 40 45
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
 50 55 60
 25 Gly Ala Val Thr Ala Pro Leu Arg Arg Val Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
 95 100 105
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Val Leu Arg Ile Pro
 140 145 150
 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
 155 160 165

35

° Phe Ala Val Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:99:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
 20 25 30
 15 His Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser
 35 40 45
 Arg Cys Trp Val His Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
 50 55 60
 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
 80 85 90
 20 Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
 95 100 105
 Gln His Ala Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Ala Thr Ala Leu Val Met Ala Gln Met Leu Arg Ile Pro
 140 145 150
 25 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 35 (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA7

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
					20					25						30
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Asn	Asn	Val	Ser	
					35					40						45
10	Arg	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Asn	Leu	
					50					55						60
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	
					65					70						75
	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85						90
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Ser	Tyr	Arg	Pro	Arg	
					95					100						105
15	Gln	His	Thr	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	
					110					115						120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145						150
	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	
					155					160						165
20	Phe	Ala	Ala	Ala	Tyr	Phe	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

25 (2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15

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Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
 20 25 30
 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Gly Asn Val Ser
 35 40 45
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
 50 55 60
 5 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Ser Pro Arg
 95 100 105
 Arg His Asn Val Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 10 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Val Val Ile Asp Ile Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Tyr Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 15 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Thr Tyr Gln Asn Ser Ser Gln Leu Tyr His Leu Thr Asn Asp
 1 10 15
 Cys Pro Asn Ser Ser Ile Val Leu Glu Ala Asp Ala Met Ile Leu
 20 25 30
 30 His Leu Pro Gln Cys Leu Pro Cys Val Arg Val Asp Asp Arg Ser
 35 40 45
 Thr Cys Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala
 50 55 60
 Ser Thr Pro Ala Thr Gln Phe Arg Arg His Val Asp Leu Leu Ala
 65 70 75
 Gln Ala Ala Val Val Cys Ser Ser Leu Tyr Ile Gln Asp Leu Cys
 80 85 90

Gln Ser Leu Phe Leu Ala Gln Gln Leu Phe Thr Phe Gln Pro Arg
 95 100 105
 Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Thr Gln
 110 115 120
 His Val Thr Gln His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 5 Ser Pro Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro
 140 145 150
 Glu Ile Cys Ala Ser Val Ile Phe Gln Gln His Trp Gln Ile Leu
 155 160 165
 Leu Ala Val Ala Tyr Phe Gln Met Ala Gln Asn Trp Leu Lys Val
 170 175 180
 Leu Ala Val Leu Phe Leu Phe Ala Gln Val Glu Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

20 ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT 78
 GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGA TTG GGT GTG CGC GCG CCG AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC 195
 CCC AAG GCA CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG 234
 25 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC 273
 GGG TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG 312
 CCT AGC TGG GGC CCC ACA GAC CCC CGG CCG AGG TCG CGC 351
 AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATA CCG CTC GTC GGC GCC CCT 429
 CTT GGA GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAC CTT 507
 CCT GGT TGC TCT TTC TCT ATC TTC CTT TTG GCC CTG CTC 546
 30 TCT TGC CTG ACC GTG CCC GCT TCG GCC 573

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
10	CCC	AAG	GCA	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
	GGG	TGG	GCG	GGA	TGG	CTG	CTG	TCT	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGC	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCG	CTC	GTC	GGC	GCC	CCT	429
	CTC	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
15	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCC	CTG	CTC	546
	TCT	TGC	CTG	ACT	GTG	CCC	GCT	TCA	GCC					573

(2) INFORMATION FOR SEQ ID NO: 105:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S14

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
30	CCC	AAG	GCA	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
	GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCT	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGC	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCG	CTC	GTC	GGC	GCC	CCC	429
35	CTC	GGG	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468

GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	CTA	GCC	CTG	CTT	546
TCT	TGC	CTG	ACT	GTG	CCC	GCT	TCA	GCC					573

(2) INFORMATION FOR SEQ ID NO: 106:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
CCC	AAG	GCG	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
GGA	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCT	CGG	312
CCT	AGC	TGG	GGC	CCT	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCT	429
CTT	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCC	CTG	CTT	546
TCT	TGC	CTG	ACA	GTG	CCC	GCG	TCA	GCC					573

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(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78

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GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGC GGT AGA CGT CAG CCT ATC 195
 CCC AAG GCG CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC 273
 GGG TGG GCG GGA TGG CTC CTG TCC CCC CGT GGC TCC CGG 312
 CCT AGC TGG GGC CCT ACA GAC CCC CGG CGT AGG TCG CGC 351
 AAT TTG GGC AAA GTC ATC GAT ACC CTC ACG TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCT 429
 CTC GGA GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAC CTT 507
 CCT GGT TGC TCT TTC TCT ATC TTC CTT CTG GCC CTG CTC 546
 TCT TGT CTG ACT GTG CCC GCG TCA GCT 573

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(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

20 ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT 78
 GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC 195
 CCC AAG GCG CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC 273
 GGG TGG GCG GGA TGG CTC CTG TCC CCC CGT GGC TCT CGG 312
 25 CCT AGC TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAC ACC CTC ACG TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTT GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGA 468
 GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAT CTT 507
 CCT GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTC 546
 TCT TGC TTG ACC GTG CCC GCA TCG GCC 573

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

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ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTC	TAT	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CAG	CCC	GAG	GGC	AGG	ACC	TGG	GCC	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TTG	273
GGG	TGG	GCA	GGA	TGG	CTC	CTG	TGA	CCC	CGT	GGC	TCT	CGG	312
CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCT	429
TTA	GGG	GGC	GCT	GCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	CGG	468
GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
CCC	GGT	TGC	CCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
TCC	TGT	TTA	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

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ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	CAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCC	GAG	CGG	TCA	CAA	CCT	CGT	GGA	CGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGC	AGG	GCC	TGG	GCC	CAG	234
CCC	GGG	CAT	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TTG	273
GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCC	CGG	312
CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
CTA	GGG	GGC	GCT	GCC	AGA	GCC	TTG	GCG	CAT	GGC	GTC	CGG	468
GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	CTG	507

CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG CTG 546
TCC TGC TTG ACC ATC CCA GGT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG 234
CCC GGG TAC CCT TGG CCC CTC TAT GGC AAC GAG GGC TTG 273
GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCC CGG 312
CCT AGT TGG GGC CCC ACC GAC CCC CGG CGT AGG TCG CGT 351
AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
CTA GGG GGT GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
GTT CTG GAG GAC GGC GTG AAT TAT GCA ACA GGG AAT TTG 507
CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG 546
TCC TGT TTG ACC ATC CCA GGT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156

TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAC GAG GGC ATG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCC CGG 312
 CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 5 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC TTG GCG CAT GGC GTC CGG 468
 GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAC TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG 546
 TCC TGT TTG ACC ATT CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 113:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 20 GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG GGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 25 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG 546
 TCC TGC CTG ACC ATC CCA GCG TCC GCT 573

30 (2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

5	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG	312
10	CCT AGT TGG GGC CCC AAC GAC CCG CGG CGT AGG TCG CGT	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAC GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG TTG	546
	TCC TGT TTG ACC ATC CCA GCT TCC GCC	573

15 (2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

25	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAG CCT ATC	195
	CCC AAG GCT CGC CAG CCC GAG GGC AGG GCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCC CGG	312
30	CCT AGT TGG GGC CCC ACA GAC CCG CGG CGT AGG TCG CGT	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GCT GCC AGG GCT CTG GCA CAT GGT GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTT TCT ATC TTC CTC TTG GCT CTG CTG	546
	TCT TGT CTG ACC ATC CCA GCT TCC GCT	573

35

CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGT TCT CGG 312
 CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAA GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 5 GTC CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAC TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTA GCT TTG CTA 546
 TCC TGT TTG ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGC CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 20 CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG 234
 CCC GGG CAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGT GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTC CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAC TTG 507
 25 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTA 546
 TCC TGT TTG ACC GTC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTC	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
5	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCA	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CAT	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAC	GGC	AAT	GAG	GGC	TTG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
10	CTA	GGG	GGC	GCT	GCC	AGG	GCT	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTC	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCT	TTG	CTG	546
	TCC	TGT	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 120:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
25	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACC	AGG	AAG	ACT	156
	TCA	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CAA	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGC	ATG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCT	CGG	312
	CCT	AAT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
30	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGT	GCC	CCC	429
	CTA	GGG	GGC	GTT	GCC	AGA	GCC	TTG	GCA	CAT	GGT	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTA	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
	TCC	TGC	TTG	ACC	ACC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 121:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

10	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACC AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGA CCC GAG GGC AGG ACC TGG GCT CAG	234
	CCC GGG TAT CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CAT GGC TCT CGG	312
	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT	351
15	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GTT GCC AGA GCC CTG GCA CAC GGT GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAC GCA ACA GGG AAT ATA	507
	CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTG	546
	TCC TGT CTG ACC ACC CCA GTT TCC GCT	573

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(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

30	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAG ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
	GGT GGC CAG ATC GTC GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CAA CCC GAG GGC AGG ACC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
35	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG	312

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CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
TTA	GGG	GGC	GTT	GCC	AGA	GCC	CTG	GCA	CAT	GGT	GTC	CGG	468
GTT	GTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	CTG	CTG	546
TCC	TGT	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

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(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

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ATG	AGC	ACG	ACT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AGC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCC	GAG	CGA	TCG	CAA	CCT	CGT	GGC	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	GCC	TGG	GCT	CAG	234
CCC	GGG	CAC	CCT	TGG	CCC	CTC	TAT	GCC	AAT	GAG	GGC	TTG	273
GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCC	CGG	312
CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GGC	CCC	429
CTA	GGG	GGC	GTT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
GTT	GTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	CTG	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCT	TTG	CTG	546
TCT	TGT	CTG	ACC	ATC	CCA	GCT	TCC	GCT					573

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(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

10	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	GAC	GAG	GGC	ATG	273
15	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCC	CGG	312
	CCT	AAT	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCT	CCC	429
	TTA	GGG	GGC	GTT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAT	TAC	GCA	ACA	GGG	AAT	TTG	507
	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
20	TCC	TGC	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

30	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	GGC	GCG	ACA	AGG	AAG	ACT	156
	TCG	GAG	CGA	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
	CCC	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
35	CCA	GGA	TAT	CCC	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGA	CTC	273

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GGC TGG GCA GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT 312
 CCC TCC TGG GGC CCC AAT GAC CCC CGG CAT AGG TCG CGC 351
 AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC AGC CTT 390
 GCC GAC CTC ATG GGG TAC GTC CCC GTC GTA GGC GGC CCG 429
 TTG GGT GGC GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA 468
 GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC TTA 507
 CCT GGT TGC TCC TTT TCT ATT TTC TTG CTG GCC CTA CTG 546
 TCC TGC ATC ACC ATT CCA GTC TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAC ACT AAC CGT CGC CCA CAA GAC GTT AAG TTT CCG GGC 78
 GGC GGC CAG ATC GTT GGC GGA GTA TAC TTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT 156
 TCG GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC ATC 195
 CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA 234
 CCA GGA TAC CCT TGG CCC CTA TAT GGG AAT GAG GGA CTC 273
 GGC TGG GCA GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT 312
 CCC TCT TGG GGC CCC ACT GAT CCC CGG CAT AGG TCG CGC 351
 AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGC TTT 390
 GCC GAC CTC ATG GGA TAC ATC CCC GTC GTG GGC GCT CCG 429
 CTT GGT GGC GTC GCC AGA GCT CTC GCG CAT GGC GTG AGG 468
 GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC TTA 507
 CCC GGT TGC TCC TTT TCT ATC TTC TTG CTG GCC TTA CTG 546
 TCC TGC ATC ACC ATT CCA GTC TCT GCT 573

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

	ATG	AGC	ACA	AAT	CCA	AAA	CCC	CAA	AGA	AAA	ACC	ATA	AGA	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	TTG	CCG	CGC	117
5	AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	ACG	ACA	AGG	AAG	ACT	156
	TCG	GAG	CGG	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
	CCC	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAC	CCC	TGG	CCT	CTA	TAT	GGG	AAT	GAG	GGA	CTC	273
	GGC	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGA	GGT	TCC	CGT	312
	CCC	TCT	TGG	GGC	CCC	AGT	GAC	CCC	CGG	CAT	AGG	TCG	CGC	351
	AAC	GTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGC	TTT	390
10	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCC	GTC	GTA	GGC	GCC	CCG	429
	CTT	GGT	GGC	GTT	GCC	AGA	GCT	CTC	GCG	CAC	GGC	GTG	AGA	468
	GTC	CTG	GAG	GAC	GGG	GTT	AAT	TAT	GCA	ACA	GGG	AAC	CTA	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	CTG	GCC	CTA	CTG	546
	TCC	TGC	ATC	ACC	ACT	CCG	GCC	TCT	GCT					573

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

	ATG	AGC	ACA	ATT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACT	AAC	CGT	CGC	CCA	CAA	GAC	GTT	AAG	TTT	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	CTG	CCG	CGC	117
25	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
	TCG	GAG	CGG	TCC	CAG	CCT	CGT	GGA	AGG	CGC	CAG	CCC	ATC	195
	CCT	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAC	CCC	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGG	CTC	273
	GGC	TGG	GCA	GGA	TGG	CTC	CTG	TCC	CCC	CGA	GGT	TCT	CGT	312
	CCC	TCT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CAT	AGG	TCG	CGC	351
	AAT	GTG	GGT	AAA	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGC	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCC	GTC	GTA	GGC	GCC	CCG	429
30	CTT	GGT	GGT	GTC	GCC	AGA	GCT	CTT	GCG	CAT	GGC	GTG	AGA	468
	GTC	CTG	GAG	GAC	GGA	GTT	AAT	TAT	GCA	ACA	GGT	AAC	TTA	507
	CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	TTG	CTA	GCC	CTG	CTG	546
	TCC	TGC	ATC	ACT	ATT	CCG	GTT	TCA	GCT					573

(2) INFORMATION FOR SEQ ID NO: 129:

35

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
10	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAT	CCT	TGG	CCT	CTT	TAC	GGA	AAC	GAG	GGC	TGC	273
	GGT	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
	CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGT	351
15	AAT	TTG	GGC	AGA	GTC	ATC	GAT	ACC	ATT	ACA	TGT	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
	GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAT	GGT	GTT	AGG	468
	GTC	CTG	GAA	GAC	GGG	ATA	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	CTT	GCT	CTT	CTG	546
	TCA	TGC	TTC	ACA	GTG	CCA	GTG	TCT	GCA					573

20 (2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
30	GGC	GGT	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAG	234
	CCA	GGA	TAT	CCT	TGG	CCT	CTG	TAC	GGA	AAC	GAG	GGC	TGC	273
	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
35	CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAC	AGA	TCA	CGT	351

AAC	TTG	GGC	AAG	GTC	ATC	GAT	ACC	ATT	ACG	TGT	GGT	TTT	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGG	468
GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
CCT	GGT	TGC	TCC	TTT	TCT	ATC	TTC	TTA	CTT	GCT	CTT	CTG	546
TCG	TGC	GCC	ACG	GTG	CCG	GTG	TCT	GCA					573

5

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

15	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAT	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	ACG	ACA	AGG	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	CCC	TGG	GGA	AAG	234
	CCA	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
20	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CAT	312
	CCT	AAT	TGG	GGC	CCC	ACT	GAC	CGC	CGG	CAT	AAA	TCA	CGC	351
	AAT	TTG	GGT	AAA	GTC	ATC	GAC	AGC	ATT	ACG	TGT	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTC	GGC	GCC	CCG	429
	GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGA	468
	GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTA	CTT	GCT	CTT	CTG	546
25	TCA	TGC	TGC	ACA	GTG	CCA	GTG	TCT	GCG					573

25

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

35

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	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAT	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
5	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAG	234
	CCA	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CAT	312
	CCT	AAT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGC	351
	AAT	TTG	GGC	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
	GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGA	468
10	GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTA	CTT	GCT	CTT	CTG	546
	TCG	TGC	TTC	ACA	GTG	CCA	GTG	TCT	GCG					573

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	TCT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
25	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCG	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
	CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGC	351
	AAT	TTG	GGC	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
	GTT	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGG	468
30	GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	TTG	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	CTT	GCT	CTT	CTG	546
	TCG	TGC	TGC	ACA	GTG	CCA	GTG	TCT	GCG					573

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACT	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCG	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAA	ACT	156
10	TCC	GAA	CGG	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
	CCT	AAA	GAT	CGG	CGC	ACC	ACT	GGC	AAG	TCC	TGG	GGA	AGG	234
	CCA	GGA	TAC	CCT	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGC	CTC	273
	GGC	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCC	CGC	GGT	TCT	CGC	312
	CCT	TCA	TGG	GGC	CCC	ACC	GAC	CCC	CGG	CAT	AAA	TCG	CGC	351
	AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCC	GTC	GTT	GGC	GCT	CCC	429
15	GTT	GGC	GGC	GTT	GCC	AGA	GCC	CTC	GCC	CAT	GGG	GTG	AGG	468
	GTT	CTG	GAG	GAC	GGG	ATA	AAT	TAT	GCA	ACG	GGG	AAT	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	CTC	TTG	GCC	CTC	TTG	546
	TCT	TGC	ATC	TCT	GTG	CCA	GTT	TCC	GCC					573

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

	ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	ATC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGC	GGA	CAG	ATC	GTT	GGT	GGA	GTA	TAC	GTG	TTG	CCG	CGC	117
	AGG	GGC	CCA	CGA	TTG	GGT	GTG	CGC	GCG	ACG	CGT	AAA	ACT	156
30	TCT	GAA	CGG	TCG	CAG	CCT	CGC	GGA	CGA	CGA	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGT	CGG	AGC	GAA	GGC	CGG	TCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGT	AAC	GAG	GGC	TGC	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCC	CCA	CGC	GGC	TCC	CGT	312
	CCA	TCT	TGG	GGC	CCA	AAC	GAC	CCC	CGG	CGA	CGG	TCC	CGC	351
	AAT	TTG	GGT	AAA	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGA	TTC	390
35	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	429

GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTC	GCG	CAT	GGC	GTG	AGG	468
GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	GGG	AAC	TTG	507
CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTT	CTT	GCT	CTG	TTC	546
TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT					573

5 (2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACC	ATC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGA	CAG	ATC	GTT	GGT	GGA	GTA	TAC	GTG	TTG	CCG	CGC	117
AGG	GGC	CCA	CGA	TTG	GGT	GTG	CGC	GCG	ACG	CGT	AAA	ACT	156
TCT	GAA	CGG	TCA	CAG	CCT	CGC	GGA	CGA	CGA	CAG	CCT	ATC	195
CCC	AAG	GCG	CGT	CGG	AGC	GAA	GGC	CGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGT	AAT	GAG	GGC	TGC	273
GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCA	CGC	GGC	TCC	CGT	312
CCA	TCT	TGG	GGC	CCA	AAC	GAC	CCC	CGG	CGG	AGG	TCC	CGC	351
AAT	TTG	GGT	AAA	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	429
GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTC	GCG	CAT	GGC	GTG	AGG	468
GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTT	GCA	ACA	GGG	AAC	TTG	507
CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTT	CTT	GCT	CTG	TTC	546
TCC	TGC	TTA	GTT	CAT	CCT	GCA	GCT	AGT					573

25 (2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
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	AAC	ACC	ATC	CGT	CGC	CCA	CAG	GAC	ATC	AAG	TTC	CCG	GGT	78
	GGC	GGA	CAG	ATC	GTT	GGT	GGA	GTA	TAC	GTG	TTG	CCG	CGC	117
	AGG	GGC	CCA	CGA	TTG	GGT	GTG	CGC	GCG	ACG	CGT	AAA	ACT	156
	TCT	GAA	CGG	TCA	CAG	CCT	CGC	GGA	CGG	CGA	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGT	CGG	AGC	GAA	GGC	CGA	TCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGT	AAC	GAG	GGC	TGC	273
5	GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCA	CGC	GGC	TCC	CGT	312
	CCA	TCT	TGG	GGC	CCA	AAT	GAC	CCC	CGG	CGG	AGG	TCC	CGC	351
	AAT	TTG	GGT	AAA	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	429
	GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTC	GCG	CAT	GGC	GTG	AGG	468
	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTT	GCA	ACA	GGG	AAC	TTG	507
	CCC	GGT	TGC	TCT	TTT	TCT	ATC	TTC	CTT	CTT	GCC	CTG	TTC	546
	TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT					573

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

20	ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	ATC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGA	CAG	ATC	GTT	GGT	GGA	GTA	TAC	GTG	TTG	CCG	CGC	117
	AGG	GGC	CCA	CGA	TTG	GGT	GTG	CGC	GCG	ACG	CGT	AAA	ACT	156
	TCT	GAA	CGG	TCA	CAG	CCT	CGC	GGA	CGG	CGA	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGT	CGG	AGC	GAA	GGC	CGG	TCC	TGG	GCT	CAG	234
	CCT	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGT	AAC	GAG	GGC	TGC	273
	GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCA	CGC	GGC	TCC	CGT	312
25	CCA	TCT	TGG	GGC	CCA	AAC	GAC	CCC	CGG	CGG	AGG	TCC	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGA	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCT	429
	GTA	GGG	GGC	GTC	GCA	AGA	GCC	CTC	GCG	CAT	GGC	GTG	AGG	468
	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	GGG	AAC	TTG	507
	CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTT	CTT	GCT	CTG	TTC	546
	TCT	TGC	CTA	ATT	CAT	CCA	GCA	GCT	AGT					573

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

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ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAC	GTA	AAG	TTC	CCG	GGT	78
GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGA	AAG	ACT	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGC	AGG	CGT	CAA	CCT	ATC	195
CCC	AAG	GCG	CGC	CAG	CCA	GAG	GGC	AGA	TCC	TGG	GCG	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCT	CCT	CGC	GGC	TCT	CGG	312
CCA	TCT	TGG	GGC	CCA	AAT	GAT	CCC	CGG	CGG	AGA	TCG	CGC	351
AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	ATC	GTG	GGC	GCC	CCC	429
GTG	GGG	GGC	GTC	GCC	AGG	GCT	CTG	GCG	CAT	GGC	GTC	AGG	468
GCT	GTG	GAG	GAC	GGG	ATT	AAC	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCA	CTT	CTT	546
TCG	TGC	CTC	ACT	GTT	CCA	GCG	TCG	GCT					573

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

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ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCT	ATG	GAT	GTA	AAA	TTC	CCA	GGC	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGC	AGG	CGT	CAG	CCT	ATC	195
CCC	AAG	GCA	CGT	CGG	TCC	GAG	GGT	AGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCA	TGG	CCT	CTT	TAC	GGT	AAT	GAA	GGC	TGT	273
GGG	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGC	TCT	CGA	312
CCG	TCT	TGG	GGC	CCA	AAT	GAT	CCC	CGG	CGG	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTG	GGC	GCC	CCA	429
GTA	GGA	GGC	GTC	GCC	AGA	GCC	CTG	GCG	CAT	GGC	GTC	AGG	468
GCT	GTG	GAG	GAC	GGG	ATC	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507

CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTT CTC 546
TCG TGC CTA ACC GTC CCA GCG TCT GCT 573

(2) INFORMATION FOR SEQ ID NO: 141:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
10 (C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
AAC ACC AAC CGT CGC CCC ATG GAT GTG AAA TTC CCG GGC 78
GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC 117
15 AGG GGC CCC CGG TTG GGT GTG CGC GCA GCT CGG AAG ACT 156
TCG GAG CGG TCA CAA CCT CGT GGC AGG CGT CAG CCT ATC 195
CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCT CAG 234
CCC GGG TAC CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT 273
GGG TGG GCA GGG TGG CTC CTG TCC CCC CGC GGT TCC AGG 312
CCG TCT TGG GGC CCC AAT GAT CCC CGG CGT AGG TCC CGT 351
AAT CTG GGT AAA GTC ATC GAT ACC CTG ACG TGT GGC TTC 390
20 GCC GAC CTC ATG GGA TAC ATT CCG CTC GTA GGC GCC CCT 429
GTG GGT GGC GTC GCC AGG GGC CTG GCG CAT GGC GTC AGG 468
GCC GTG GAG GAC GGA ATT AAC TAC GCA ACA GGG AAC CTT 507
CCT GGT TGC TCT TTC TCT ATC TTT CTT CTT GCA CTT CTC 546
TCG TGC CTG ACA ACA CCA GCA TCT GCC 573

(2) INFORMATION FOR SEQ ID NO: 142:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
30 (C) INDIVIDUAL ISOLATE: Z5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
AAC ACC AAC CGC CGC CCC ATG GAT GTA AAA TTC CCG GGT 78
GGT GGT CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC 117
35 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT 156

TCG GAG CGG TCG CAA CCT CGC GGC AGG CGT CAG CCT ATC 195
 CCC CAG GCA CGT CGG TCC GAG GGC AGG TCC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCT CTT TAT GGC AAT GAG GGC TGT 273
 GGG TGG GCA GGG TGG CTC CTG TCC CCC CGC GGA TCT CGG 312
 CCA TCT TGG GGC CAA AAT GAT CCC CGG CGT AGG TCC CGC 351
 AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGT GGC TTC 390
 5 GCC GAC CTC ATG GGA TAC ATT CCG CTC GTC GGC GCC CCA 429
 GTA GGT GGC GTC GCC AGG GCC TTG GCG CAT GGC GTC AGG 468
 GCC CTG GAG GAC GGA ATC AAC TAT GCA ACA GGG AAT CTT 507
 CCT GGT TGC TCC TTT TCT ATC TTC CTA CTT GCA CTT TTC 546
 TCG TGC TTG ACA ACA CCG GCA TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 143:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT 78
 GGT GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC 117
 20 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCG GAG CGG TCG CAA CCT CGT GGG AGA CGC CAG CCT ATC 195
 CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG 234
 CCC GGG TAT CCA TGG CCT CTT TAC GGT AAT GAG GGT TGC 273
 GGG TGG GCG GGA TGG CTC CTG TCA CCC CGT GGC TCT CGA 312
 CCG TCT TGG GGT CCA AAT GAT CCC CGG CGA AGG TCC CGC 351
 AAC TTG GGT AAG GTC ATC GAT ACT CTA ACT TGC GGT TTC 390
 25 GCC GAT CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC CCC 429
 GTG GGC GGC GTC GCC AGG GGC CTG GCA CAT GGT GTT AGG 468
 GCT GTG GAG GAC GGG ATC AAT TAT GCA ACA GGG AAT CTT 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTT CTT 546
 TCG TGC CTA ACT GTT CCC ACC TCG GCC 573

(2) INFORMATION FOR SEQ ID NO: 144:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

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(2) INFORMATION FOR SEQ/ ID NO: 145:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	ATG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGG	AGG	CGC	CAG	CCT	ATC	195
CCC	AAG	GCG	CGC	CAA	CTC	GAG	GGT	AGG	TCC	TGG	GCT	CAG	234
CCT	GGG	TAT	CCT	TGG	CCC	CTT	TAC	GGC	AAT	GAG	GGC	TGC	273
GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGG	312
CCG	TCT	TGG	GGC	CCG	AAT	GAT	CCC	CGG	CGG	AGG	TCC	CGC	351
AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACT	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	GTC	GTA	GGC	GCC	CCC	429
GTG	GGT	GGC	GTC	GCC	AGA	GCC	CTG	GCG	CAT	GGC	GTC	AGG	468
CTT	CTG	GAG	GAC	GGG	GTC	AAT	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCA	CTG	CTC	546
TCG	TGC	CTG	ACT	GTT	CCC	GCT	TCG	GCC					573

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

10	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTC TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
15	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	429
	GTT GGG GGC GTC GCA AGG GCC CTT GCA CAT GGT GTG AGG	468
	GTT CTT GAG GAC GGG GTA AAC TAT GCA ACG GGG AAT TTG	507
	CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC	546
20	TCG TGC CTG ACC GTC CCG GCC TCT GCA	573

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

30	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGA TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234

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CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC 273
 GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG 312
 CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAA TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCC CTC GCA CAT GGT GTG AGG 468
 GTT CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTG 507
 5 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC 546
 TCG TGC TTG ACC GTC CCA GCC TCT GCA 573

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT 156
 TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT 195
 20 CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA 234
 CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC 273
 GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG 312
 CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAG TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAC ACC CTA ACA TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG 468
 GTT CTT GAG GAC GGG GTA AAT TAC GCA ACA GGG AAT CTG 507
 25 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC 546
 TCG TGC CTG ACC GTC CCA GCC TCC GCA 573

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CTC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
5	TCG	GAA	CGG	TCG	CAA	CCC	CGT	GGG	CGG	CGC	CAG	CCT	ATT	195
	CCC	AAG	GCG	CGC	CAA	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GGG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
	CCT	AAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGG	AAG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
10	GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	468
	GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAC	GCA	ACA	GGG	AAT	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	ATC	CTT	GCA	CTT	CTT	546
	TCC	TGT	CTG	ATC	ATC	CCG	GCC	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
25	TCA	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGC	CAG	CCT	ATT	195
	CCC	AAG	GCT	CGC	CAG	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GAG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	AAC	GAC	CCC	CGG	CGG	AAA	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
	GCC	GAT	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
30	GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAT	GGT	GTG	AGG	468
	GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAC	GCA	ACA	GGG	AAT	TTA	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	ATC	CTT	GCA	CTT	CTT	546
	TCA	TGC	CTG	ACC	GTC	CCG	GCC	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 151:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
10	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	GCA	ACT	CGG	AAG	ACT	156
	TCA	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGT	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGC	CAG	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAT	GCC	AAT	GAG	GGC	CTC	273
	GGG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
	CCT	AAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGG	AAA	TCG	CGC	351
15	AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGC	GGA	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
	GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	468
	GTC	CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTA	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	ATC	CTT	GCA	CTT	CTT	546
	TCA	TGC	CTG	ACT	GTC	CCG	ACC	TCT	GCC					573

20 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	CAA	AGA	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
30	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	CGT	ATG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
	TCG	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGT	CAG	CCT	ATT	195
	CCC	AAG	GCG	CGC	CAA	TCC	GCG	GGT	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GGG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
35	CCT	AAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGA	AAA	TCG	CGC	351

AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	468
GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	GTC	CTT	GCA	CTT	CTC	546
TCG	TGC	CTA	ACC	GTC	CCT	GCC	TCT	GCA					573

5 (2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
TCA	GAA	CGG	TCG	CAA	CCC	CGT	GGG	CGG	CGT	CAG	CCT	ATT	195
CCC	AAG	GCG	CGC	CAA	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
CCC	GGG	TAC	CCT	TGG	CCC	TTT	TAC	GCC	AAT	GAG	GGC	CTC	273
GGG	TGG	GCA	GGG	TGG	CTG	CTC	TCC	CCT	CGA	GGC	TCT	CGG	312
CCT	AAC	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGA	AGA	TCG	CGC	351
AAT	TTG	GGC	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
GTT	GGG	GGC	GTC	GCA	AGG	GCC	CTC	GCA	CAC	GGT	GTG	AGA	468
GCT	CTT	GAG	GAC	GGG	GTA	AAT	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTC	TCC	ATC	TTT	ATC	CTT	GCA	CTT	CTC	546
TCG	TGC	TTG	ACC	GTC	CCG	GCC	ACT	GCA					573

25 (2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

ATG	AGC	ACA	CTT	CCA	AAA	CCC	CAA	AGA	AAA	ACC	AAA	AGA	39
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

35

	AAC	ACC	AAC	CGT	CGC	CCA	ACG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	CGG	TTG	GGT	GTG	CGC	GCG	ACG	AGA	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCC	AGA	GGC	AGG	CGC	CAA	CCT	ATA	195
	CCA	AAG	GCG	CGC	CAG	CCC	CAG	GGC	AGG	CAC	TGG	GCT	CAG	234
	CCC	GGA	TAC	CCT	TGG	CCT	CTT	TAT	GGA	AAC	GAG	GGC	TGT	273
5	GGG	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGC	TCC	CGG	312
	CCA	CAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGT	CGA	TCC	CGG	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGT	GGG	TTC	390
	GCC	GAT	CTC	ATG	GGG	TAC	ATT	CCC	GTC	GTG	GGC	GCG	CCT	429
	TTG	GGC	GGC	GTC	GCG	GCT	GCG	CTC	GCA	CAT	GGC	GTG	AGG	468
	GCA	ATC	GAG	GAC	GGG	ATC	AAT	TAT	GCA	ACA	GGG	AAT	CTC	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCA	CTA	CTC	546
10	TCG	TGC	CTC	ACA	ACG	CCA	GCT	TCG	GCT					573

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

20	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
25	Arg	Leu	Gly	Val	Arg	Ala	Pro	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
30	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	105				110					115				
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
35	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	150													

000491.02593

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

35

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
20	105				110					115				
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	150				155					160				
25	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	165				170					175				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	180				185					190				
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

5 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 10 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 15 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 20 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

35 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10

Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 5 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 10 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 15 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 160:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 30 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70

Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 10 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 161:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 (vi) ORIGINAL SOURCE:
 20 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA10
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 25 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 30 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 35

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 5 Leu Pro Gly Cys Pro Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 162:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Ser Thr Asn Pro Lys Pro Gln Arg Ala Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 25 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 30 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180

Ser Cys Leu Thr Ile Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 163:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60 65 70
Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
20 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
25 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170 175 180
30 Ser Cys Leu Thr Ile Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 164:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5			10						
Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
15				20			25						
Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
30				35			40						
Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
45				50			55						
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
60				65			70						
Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
75				80			85						
Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	Leu	Leu
90				95			100						
Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
105				110			115						
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
120				125			130						
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
135				140			145						
Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
150				155			160						
Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
165				170			175						
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
180				185			190						
Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 5 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 10 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 15 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190
 20

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 35

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Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 10 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

25 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 35 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95

Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

35

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	His	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
20	105				110					115				
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	150				155					160				
25	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	165				170					175				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	180				185					190				
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

5 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
10 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg His
60 65 70
Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110
15 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
20 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170 175 180
Ser Cys Leu Thr Ile Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 172:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

35 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10

° Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
60 65 70
5 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Thr Asp Pro
100 105 110
10 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
15 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170 175 180
Ser Cys Leu Thr Thr Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 173:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
25 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60 65 70

35

Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 5 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Ile Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Leu Thr Thr Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125

35

° Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Val Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 5 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 15 (C) INDIVIDUAL ISOLATE: P8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Met	Ser	Thr	Thr	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5					10				
Thr	Ser	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
15					20					25			
Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
20						35					40		
Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45					50					55	
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
			60					65				70	
Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	His	Pro	Trp	Pro
			75						80				
25	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu
	85				90					95			
Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115					120					125	
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
			130					135					140
30	Gly	Gly	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His
					145					150			
Val	Arg	Val	Val	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
155					160					165			
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170					175					180		

° Ser Cys Leu Thr Ile Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5					10				
Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
15					20					25			
Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
15		30				35				40			
Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45				50						55	
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
		60						65				70	
Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
			75					80					
20	Leu	Tyr	Gly	Asp	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	Leu
	85				90					95			
Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
	100				105					110			
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115				120					125		
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
		130						135				140	
25	Gly	Ala	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His
			145					150					
Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
155				160					165				
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170				175						180		
Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
30		185					190						

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T4

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
10		30				35				40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45				50				55				
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
		60				65				70				
	Ser	Thr	Gly	Lys	Ser	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
		75				80				85				
15	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
		100				105				110				
	Arg	His	Arg	Ser	Arg	Asn	Val	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115				120				125				
	Thr	Cys	Ser	Leu	Ala	Asp	Leu	Met	Gly	Tyr	Val	Pro	Val	Val
		130				135				140				
20	Gly	Gly	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
		145				150				155				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
		160				165				170				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		175				180				185				
	Ser	Cys	Ile	Thr	Ile	Pro	Val	Ser	Ala					
		185				190								

25 (2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

35

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Thr Ile Pro Val Ser Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

30

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Ile Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Thr Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55

35

Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 5 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 10 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 30 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110

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(i)

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(xi)

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Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Phe Thr Val Pro Val Ser Ala
 185 190

5 (2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 15 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 20 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 25 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 30 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ala Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 183:

35

09084691.052698

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
10	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35					40		
	Arg	Leu	Gly	Val	Arg	Thr	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
				60					65					70
15	Ser	Thr	Gly	Lys	Pro	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
		85				90					95			
	Ser	Pro	Arg	Gly	Ser	His	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
		100					105					110		
	Arg	His	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Ile
			115					120				125		
20	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val
				130					135					140
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
		155				160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
25							175						180	
	Ser	Cys	Cys	Thr	Val	Pro	Val	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 184:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

35

(C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
5	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35				40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
				60						65				70
10	Ser	Thr	Gly	Lys	Ser	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90					95			
	Ser	Pro	Arg	Gly	Ser	His	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
		100					105					110		
	Arg	His	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Ile
			115					120					125	
15	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val
				130						135				140
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
	155					160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170					175					180		
20	Ser	Cys	Phe	Thr	Val	Pro	Val	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			

° Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Ser Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 10 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 15 Ser Cys Cys Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

30 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly Tyr Pro Trp Pro
 75 80

Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110
Arg His Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
5 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
130 135 140
Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
155 160 165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170 175 180
10 Ser Cys Ile Ser Val Pro Val Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
25 Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60 65 70
Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
30 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
35 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140

Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 5 Ser Cys Leu Ile His Pro Ala Ser
 185 190

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 Ser Cys Leu Val His Pro Ala Ala Ser
 185 190

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(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK12

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5					10				
Thr	Ile	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
15					20				25				
Gln	Ile	Val	Gly	Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro
	30				35				40				
10	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg
		45			50				55				Ser
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
		60						65				70	
Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
			75					80					
Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
85				90					95				
15	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp
		100				105					110		Pro
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115				120					125		
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
			130					135				140	
Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
			145					150					
20	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly
		155			160					165			Asn
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe
		170			175					180			
Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser					
		185					190						

25 (2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

30 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

35

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 10 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Ile Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 15 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

20 (2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55

35

° Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60 65 70
Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110
5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
155 160 165
10 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170 175 180
Ser Cys Leu Thr Val Pro Ala Ser Ala
185 190

15 (2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
25 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Ala Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60 65 70
30 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

35

° Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 5 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 194:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 20 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Gln Ala Arg Arg
 60 65 70
 25 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Gln Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 30 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165

35

° Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 195:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 15 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 20 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 25 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 30 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Thr Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 196:

35

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5			10						
Thr	Asn	Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
15				20			25						
Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30			35			40						
Arg	Leu	Gly	Val	Arg	Thr	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45			50			55						
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60			65			70						
Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75			80			85						
Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
85			90				95						
Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	100			105			110						
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	115			120			125						
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	130			135			140						
Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
	145			150			155						
Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
155			160				165						
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170		175				180						
Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					
	185			190									

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Leu Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Leu Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25

° Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
60 65 70
Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
75 80
5 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110
Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
10 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
170 175 180
15 Ser Cys Leu Thr Val Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
20 (C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

25 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
60 65 70
Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
75 80
35 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
85 90 95

Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Leu Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Ile Ile Pro Ala Ser Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30					35				40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45					50				55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Gln
	60								65					70
	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75								80					
	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Glu	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	100					105						110		
20	Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	115							120				125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	130							135				140		
	Gly	Gly	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
	145							150						
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
25	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu
	170					175					180			
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					
	185					190								

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35				40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45					50					55		
10	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Gln
			60						65				70	
	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
				75						80				
	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90				95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
	100						105				110			
15	Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120				125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135				140	
	Gly	Gly	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
20	155					160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu
		170					175				180			
	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser	Ala					
			185				190							

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Gln	Arg	Asn
1				5					10				

5 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Met Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 10 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Ser Ala Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 15 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 20 Leu Pro Gly Cys Ser Phe Ser Ile Phe Val Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 205:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA11

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

 30 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 35 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70

Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Phe Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 10 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Thr Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Thr Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Gln Gly Arg His Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro His Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125

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° Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Ala Ala Leu Ala His Gly
 145 150
 Val Arg Ala Ile Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 5 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:207:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

15 GCGTCCGGGT TCTGGAAGAC GCGTGAACT ATGCAACAGG 40

(2) INFORMATION FOR SEQ ID NO:208:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

25 AGGCTTTCAT TGCAGTTCAA GGCCGTGCTA TTGATGTGCC 40

(2) INFORMATION FOR SEQ ID NO:209:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

35 AAGACGGCGT GAACTATGCA ACAGGGAACC TTCCTGGTTG 40

(2) INFORMATION FOR SEQ ID NO:210:

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09084691.052698

- 0
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:
AGTTCAAGGC CGTGCTATTG ATGTGCCAAC TGCCGTTGGT 40
- (2) INFORMATION FOR SEQ ID NO:211:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:
15 AAGACGGCGT GAATTCTGCA ACAGGGAACC TTCCTGGTTG 40
- (2) INFORMATION FOR SEQ ID NO:212:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:
AGTTCAAGGC CGTGGAATTC ATGTGCCAAC TGCCGTTGGT 40
- 25 (2) INFORMATION FOR SEQ ID NO:213:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:
ARCTYCGACG TYACATCGAY CTGCTYGTYG GRAGYGCCAC CC 42
- (2) INFORMATION FOR SEQ ID NO:214:
- 35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:
 GATGCGCGTT CCCGAGGTCA TCWTAGACAT CRTYRGCGGR GCD 43

(2) INFORMATION FOR SEQ ID NO:219:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:
 15 AATGGCACCY TGCRCCTGCTG GATACAAGTR ACACCTAATG TGGCTGTGAA 50
 ACAC 54

(2) INFORMATION FOR SEQ ID NO:220:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:
 25 TGARCTAGYC CTYSARGTYG TCTTCGGYGG Y 31

(2) INFORMATION FOR SEQ ID NO:221:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:
 35 GCCAACGTCT CTCGATGTTG GGTGCCGGTT GCCCCCAATC TCGCCATAAG 50
 TCAA 54

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AAGGGCCTGC GAGCACACAT CGATATCATC GTGATGTCTG CTACGG 46

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TTGGTGCGCA TCCCGGAAGT CATCTTGGAT ATTGTTACAG GAGGT 45

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

AGTCAGGTAY GTCGGAGCAA CCACCGCYTC GATACGCAGT 40

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGCCTTCACG TTCAGACCKC GTCGCCATCA AACRGTCAG ACCTGT 46

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TCCCCCGCYG TGGGTATGGT GGTRGCGCAC RTYCTGCGDY TGCCCCAGAC 50
CKTGTTYGAC ATAMTRGCGY GGGCC 75

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ACGCCGGTGA CGCCTACAGT GGCTGTCGCA CACCCGGGC 39

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ATGAGGGTCC CCACAGCCTT TCTCGACATG GTTGCCGGAG GC 42

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGCGCCCTAT CCAACGCAC CGTTAGAGTC CATGCGCAGG 40

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TCAGATCTTA CGGATCCCCT CTATCCTAGG TGA CT TGCTC ACCGGGGGT 49

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CAGTCACGCT GCTGGGTGGC CCTTACTCCC ACCGTGGCGG YGYCTTATAT 50
CGGT 54

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

TAGCACTCTG GTRGAYCTAC TCRCTGGAGG G 31

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

AAGTCTACAT GCTGGGTGTC TCTACCCCC ACCGTGGCTG CGCAACATCT 50

54

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(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TCTTCTTGCG GCGCCGCAG TGGTTTGCTC ATCCCTG 37

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

ATCTAGCATC TTGAGGGTAC CTGAGATTG TGCGAGTGTG ATATTGGTG 50
 GC 52

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	Gly	Ala
					5				10					15
Leu	Thr	His	Asn	Leu	Arg	Xaa	His	Xaa	Asp	Xaa	Ile	Val	Met	Ala
				20					25					30
Ala	Thr	Val												

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro Gly Ala
5 10 15
Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val Met Ser
20 25 30
5 Ala Thr Val

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Trp Ile Pro Val Xaa Pro Asn Val Ala Val Xaa Xaa Pro Gly Ala
5 10 15
Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val Met Ser
20 25 30
Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Trp Thr Xaa Val Thr Pro Thr Val Ala Val Arg Tyr Val Gly Ala
5 10 15
Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly Ala
20 25 30
Ala Thr Xaa

30 (2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Trp Val Ala Leu Xaa Pro Thr Leu Ala Ala Arg Asn Xaa Xaa Xaa
 5 10 15
 Xaa Thr Xaa Xaa Ile Arg Xaa His Val Asp Leu Leu Val Gly Ala
 20 25 30
 Ala Xaa Phe

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Trp Val Xaa Xaa Xaa Pro Thr Val Ala Thr Arg Asp Gly Lys Leu
 5 10 15
 Pro Xaa Xaa Gln Leu Arg Arg Xaa Ile Asp Leu Leu Val Gly Ser
 20 25 30
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro Gly Ala
 5 10 15
 Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala
 20 25 30
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Trp Val Ala Leu Thr Pro Thr Val Ala Xaa Xaa Tyr Ile Gly Ala
 5 10 15
 Pro Leu Xaa Ser Xaa Arg Arg His Val Asp Leu Met Val Gly Ala
 20 25 30
 Ala Thr Val

5 (2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu Asn Ala
 5 10 15
 Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val Gly Gly
 20 25 30
 Ala Thr Leu

15 (2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Pro Asn Ala
 5 10 15
 Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala
 20 25 30
 Ala Thr Met

25 (2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Trp Val Xaa Ile Thr Pro Thr Leu Ser Ala Pro Xaa Xaa Gly Ala
 5 10 15
 Val Thr Ala Pro Leu Arg Arg Xaa Val Asp Tyr Leu Ala Gly Gly
 20 25 30
 Ala Ala Leu

(2) INFORMATION FOR SEQ ID NO:251:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

10 Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala Ser Thr
 5 10 15
 Pro Ala Thr Gly Phe Arg Arg His Val Asp Leu Leu Ala Gly Ala
 20 25 30
 Ala Val Val

15 (2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu
 5 10 15
 Xaa Leu Xaa Val Val Phe Gly Gly
 20

25 (2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro Glu Val
 5 10 15
 Ile Leu Asp Ile Val Thr Gly Gly
 20

35

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Thr Xaa Thr Xaa Ile Leu Ala Tyr Xaa Met Arg Val Pro Glu Val
 5 10 15
Ile Xaa Asp Ile Xaa Xaa Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Ala Val Gly Met Val Val Ala His Xaa Leu Arg Leu Pro Gln Thr
 5 10 15
Xaa Phe Asp Ile Xaa Ala Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Thr Xaa Ala Leu Val Xaa Ser Gln Leu Leu Arg Xaa Pro Gln Ala
 5 10 15
Xaa Xaa Asp Xaa Val Xaa Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

5 Thr Xaa Ala Leu Val Xaa Ala Gln Leu Leu Arg Xaa Pro Gln Ala
5 10 15
Xaa Leu Asp Met Ile Ala Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:258:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

15 Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro Thr Ala
5 10 15
Phe Leu Asp Met Val Ala Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:259:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

25 Thr Thr Thr Leu Xaa Leu Ala Gln Val Met Arg Ile Pro Ser Thr
5 10 15
Leu Val Asp Leu Leu Xaa Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:260:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

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Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro Gly Ala
 5 10 15
 Met Val Asp Leu Leu Ala Gly Gly
 20

5 (2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro Ser Ile
 5 10 15
 Leu Gly Asp Leu Leu Thr Gly Gly
 20

15 (2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Xaa Thr Ala Leu Xaa Met Ala Gln Xaa Leu Arg Ile Pro Gln Val
 5 10 15
 Val Ile Asp Ile Ile Ala Gly Xaa
 20

25 (2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro Glu Ile
 5 10 15
 Cys Ala Ser Val Ile Phe Gly Gly
 20

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